

STIC-Biotech/ChemLib

125082

From: Hamud, Fozia  
Sent: Tuesday, December 27, 2005 12:34 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 10/691,923

Hello,  
Kindly search SEQ ID NO:34 of 10/691,923 against commercial and interference data bases. Thank you.

FOZIA HAMUD  
PATENT EXAMINER  
ART UNIT 1647  
ROOM:REM 4D64  
MAIL BOX: REM 4C70

CRFF

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 13:46:42 ; Search time 227 Seconds  
(without alignments)  
565.666 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGVPVTSKPTTGTGKGCHGR.....LKTVADGNLSLRTSTHPST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	945	99.0	200	1	IL29 HUMAN	Q81u54 homo sapien
2	667.5	69.9	200	1	IL28B HUMAN	Q81z19 homo sapien
3	653.5	68.4	200	1	IL28A HUMAN	Q81zj0 homo sapien
4	477	49.9	193	2	Q4VK74 MOUSE	Q4vk74 mus musculu
5	463	48.5	193	2	Q4VK73 MOUSE	Q4vk73 mus musculu
6	458	48.0	193	1	IL28 MOUSE	Q8cgk6 mus musculu
7	97.5	10.2	692	1	PPK ACIBA	Q9x4m8 acinetobact
8	89.5	9.4	914	2	Q4ZV84 PSESY	Q4zv84 pseudomonas
9	89	9.3	296	2	Q8G5G0 BIFLO	Q8g5g0 bifidobacte
10	89	9.3	458	2	Q8DJLO SYNEL	Q8dj10 synecococc
11	88.5	9.3	313	2	Q75BW8 ASHGO	Q75bw8 ashbya goss
12	87.5	9.2	953	2	Q6FCX8 ACTAD	Q6fcx8 acinetobact
13	87	9.1	479	2	Q7QZJ8 GIALA	Q7qzj8 giardia lam
14	86.5	9.1	967	2	Q5B9M4 EMENI	Q5b9m4 aspergillus
15	86	9.0	333	2	Q58D46 BOVIN	Q58d46 bos taurus
16	86	9.0	528	2	Q4KB02 PSEF5	Q4kb02 pseudomonas
17	86	9.0	567	2	Q5EA80 BOVIN	Q5ea80 bos taurus
18	85.5	9.0	574	2	Q52GV5 MAGGR	Q52gv5 magnaporthe
19	85.5	9.0	2173	2	Q4C895 LEIMA	Q4c895 leishmania
20	85	8.9	673	2	Q57P05 SALCH	Q57pj5 salmonella
21	85	8.9	975	2	Q4C6E0 LEIMA	Q4c6e0 leishmania
22	84.5	8.8	371	2	Q6SP70 9RETR	Q6sp70 small rumin
23	84.5	8.8	455	2	Q9SG79 ARATH	Q9sg79 arabidopsis
24	84.5	8.8	881	2	Q60AC8 METCA	Q60ac8 methylococc
25	84.5	8.8	918	2	Q884J3 PSESM	Q884j3 pseudomonas
26	84.5	8.8	1122	2	Q8J4V1 9RETR	Q8j4v1 visha/maedi
27	84.5	8.8	1799	1	DOCK8 HUMAN	Q8nf50 homo sapien
28	84.5	8.8	2032	2	Q5JPJ1 HUMAN	Q5jpp1 homo sapien
29	84	8.8	204	2	Q88N24 PSEPK	Q88n24 pseudomonas
30	84	8.8	663	2	Q9NV65 HUMAN	Q9nv65 homo sapien
31	84	8.8	1379	2	Q7QEK5 ANOGA	Q7qek5 anopheles g

32 83.5 8.7 414 2 Q69TN3 ORYSA  
33 83.5 8.7 499 2 Q4FBH3 ECOLI  
34 83.5 8.7 597 2 Q7ULZ9 RHOPA  
35 83.5 8.7 716 2 Q6C489 YARLI  
36 83.5 8.7 1470 2 Q8CHD4 MOUSE  
37 83 8.7 567 1 PGTA HUMAN  
38 83 8.7 567 2 Q6FHF7 HUMAN  
39 83 8.7 567 2 Q5NVK5 PONPY  
40 83 8.7 739 2 Q8BI71 MOUSE  
41 83 8.7 889 2 Q8DLK6 SYNEL  
42 82.5 8.6 1443 2 Q4T8K2 TETNG  
43 82.5 8.6 3317 2 Q9RAH2 9NOSO  
44 82 8.6 315 1 SPY2 MOUSE  
45 82 8.6 899 1 PRP6\_YEAST

## ALIGNMENTS

RESULT 1  
ID IL29 HUMAN STANDARD; PRT; 200 AA.  
AC Q81U54;  
DT 01-FEB-2005 (Rel. 46, Created)  
DT 01-FEB-2005 (Rel. 46, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Interleukin 29 precursor (IL-29) (Interferon lambda-1) (IFN-lambda-1)  
DE (Cytokine ZCYTO21).  
GN Name=IL29; Synonyms=IFNL1, ZCYTO21;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=12469119; DOI=10.1038/ni873;  
RA Sheppard P., Kindvogel W., Xu W., Henderson K., Schlutsmeyer S.,  
RA Whitmore T.E., Kuestner R., Garrigue U., Birks C., Roraback J.,  
RA Ostrander C., Dong D., Shin J., Presnell S., Fox B., Haldeman B.,  
RA Cooper E., Taft D., Gilbert T., Grant F.J., Tackett M., Krivan W.,  
RA McKnight G., Clegg C., Foster D., Klucher K.M.;  
RA "IL-28, IL-29 and their class II cytokine receptor IL-28R.";  
RL Nat. Immunol. 4:63-68(2003).  
RT [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=12483210; DOI=10.1038/ni875;  
RA Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,  
RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;  
RA "IFN-lambdas mediate antiviral protection through a distinct class II  
cytokine receptor complex.";  
RL Nat. Immunol. 4:69-77(2003).  
RT [3]  
RP NUCLEOTIDE SEQUENCE.  
Li M., He S.;  
RT "Construction of mammalian cell expression vector of human interleukin  
(IL)-28A, IL-28B and IL-29 gene from activated peripheral blood  
mononuclear cell and analysis of its sequence.";  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RT [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Cytokine with immunomodulatory activity. May play a role
CC in antiviral immunity. Up-regulates MHC class I antigen
CC expression. Ligand for the heterodimeric class II cytokine
CC receptor composed of IL10RB and IL28RA. The ligand/receptor
CC complex seems to signal through the Jak-STAT pathway.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By viral infections or double stranded RNA.
CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY129150; AAN28265.1; -; mRNA.
CC EMBL; AY184372; AAN86125.1; -; mRNA.
CC EMBL; AY336716; AAR24511.1; -; mRNA.
CC EMBL; BC074985; AAR74985.1; -; mRNA.
CC Ensembl; ENSG00000182393; Homo sapiens.
CC HGNC; HGNC:18363; IL29.
CC MIM; 607403; -.
CC Antiviral defense; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 19 Potential.
CC CHAIN 20 200 Interleukin 29.
CC CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 200 AA; 21898 MW; D4433B9462DCB41 CRC64;
Query Match 99.0%; Score 945; DB 1; Length 200;
Best Local Similarity 99.4%; Pred. No. 2.4e-78;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GVPVTSKPTTTGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPNGWDL 61
Db 20 GVPVTSKPTTTGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPNGWDL 79
Qy 62 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPTAG 121
Db 80 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPTAG 139
Qy 122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 181
Db 140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 199
Qy 182 T 182
Db 200 T 200
RESULT 2
ID IL28B HUMAN STANDARD; PRT; 200 AA.
AC Q81Z19; Q6VNS6; Q7ZAJ3; Q81WL6;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin 28B precursor (IL-28C) (Interferon lambda-3)
DE (IFN-lambda-3) (Interferon lambda-4) (IFN-lambda-4) (Cytokine
DE ZCYTO22).
GN Name=IL28B; Synonyms=IFNL3, IFNL4, IL28C, ZCYTO22;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.
RX PubMed=12469119; DOI=10.1038/nr1873;
RA Sheppard P., Kindevogel W., Xu W., Henderson K., Schlutemeyer S.,
RA Whitmore T.E., Kuestner R., Garrigues U., Birks C., Roraback J.,
RA Ostrander C., Dong D., Shin J., Prensell S., Fox B., Haldeman B.,
RA Cooper E., Taft D., Gilbert T., Grant P.J., Tackett M., Krivan W.,
RA McKnight G., Clegg C., Foster D., Klucher K.M.;
RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";
RL Nat. Immunol. 4:63-68 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 5-200, FUNCTION, SUBCELLULAR LOCATION, AND
RP INDUCTION.
RX PubMed=12483210; DOI=10.1038/nr1875;
RA Kotenko S.V., Gallagher G., Bauzin V.V., Lewis-Antes A., Shen M.,
RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;
RT "IFN-lambda mediate antiviral protection through a distinct class II
RT cytokine receptor complex.";
RL Nat. Immunol. 4:69-77 (2003).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 4-200.
RA Li M., He S.;
RT "Construction of mammalian cell expression vector of human interleukin
RT IL-29, IL-28A, IL-28B and IL-28C gene from activated peripheral blood
RT mononuclear cell and analysis of its sequence.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine with immunomodulatory activity. May play a role
CC in antiviral immunity. Up-regulates MHC class I antigen
CC expression. Ligand for the heterodimeric class II cytokine
CC receptor composed of IL10RB and IL28RA. The ligand/receptor
CC complex seems to signal through the Jak-STAT pathway.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By viral infections or double stranded RNA.
CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY129149; AAN28264.1; -; mRNA.
CC EMBL; AY184374; AAN86127.1; -; mRNA.
CC EMBL; AY336714; AAR24509.1; ALT_INIT; mRNA.
CC EMBL; AY336717; AAO01561.1; ALT_INIT; mRNA.
CC Ensembl; ENSG00000197110; Homo sapiens.
CC HGNC; HGNC:18365; IL28B.
CC MIM; 607402; -.
CC Antiviral defense; Cytokine; Signal.
CC SIGNAL 1 25 Potential.
CC CHAIN 26 200 Interleukin 28B.
CC CONFLICT 74 74 K -> R (in Ref. 3; AAO01561).
CC CONFLICT 112 112 T -> S (in Ref. 2).
CC CONFLICT 124 124 D -> G (in Ref. 3; AAO01561).
CC CONFLICT 159 159 L -> P (in Ref. 3; AAO01561).
CC CONFLICT 160 160 H -> Y (in Ref. 2).
CC SEQUENCE 200 AA; 22194 MW; 4DD71C5DAC6D7E66 CRC64;
Query Match 69.9%; Score 667.5; DB 1; Length 200;
Best Local Similarity 76.6%; Pred. No. 6.3e-53;
Matches 134; Conservative 11; Mismatches 25; Indels 5; Gaps 2;
Qy 2 GVPVTSK---PTTGTGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPNGN 58
Db 24 GAVPEVARLRGALPDARGCHTAQFKSLSPQELAQFGRKADAEESLLKDKCKRSLRFPRT 83
Qy 59 WDLRLQLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQP 116
Db 84 WDLRLQLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQP 143
Qy 117 QPTAGPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTLRLKYVADGNL 171
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144 OPTAGPRTGRGLHHHLHRLQAPKRESGCLASVTNLFLLTRDLNCVASGDL 198

Db

RESULT 3

IL28A HUMAN STANDARD; PRT; 200 AA.

AC QRIZJO; QGVN55; Q8TWL7;

DT 01-FEB-2005 (Rel. 46, Created)

DT 01-FEB-2005 (Rel. 46, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Interleukin 28A precursor (IL-28A) (Interferon lambda-bda-2) (Cytokine ZCYTO20).

DE 2) (Cytokine ZCYTO20).

GN Name=IL28A; Synonyms=IFNL2, ZCYTO20;

OS Homo sapiens (Human).

OC Sakurayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

OX [1]

RN NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.

RX PubMed=12469119; DOI=10.1038/nl873;

RA Sheppard P., Kindsvogel W., Xu W., Henderson K., Schlutsmeyer S., Whitmore T.E., Kuestner R., Garrigues U., Birks C., Roraback J., Ostrand C., Dong D., Shin J., Presnell S., Fox B., Haldeman B., Cooper E., Taft D., Gilbert T., Grant F.J., Tackett M., Krivan W., McKnight G., Clegg C., Foster D., Klucher K.M.;

RA "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RT Nat. Immunol. 4:63-68(2003).

RN [2]

RN NUCLEOTIDE SEQUENCE OF 5-200, FUNCTION, SUBCELLULAR LOCATION, AND INDUCTION.

RP PubMed=12483210; DOI=10.1038/nl875;

RP Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M., Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;

RA "IFN-lambdas mediate antiviral protection through a distinct class II cytokine receptor complex.";

RT Nat. Immunol. 4:69-77(2003).

RN [3]

RN NUCLEOTIDE SEQUENCE OF 4-200.

RA Li M., He S.;

RA "Construction of mammalian cell expression vector of human interleukin (IL)-28A, IL-28B and IL-29 gene from activated peripheral blood mononuclear cell and analysis of its sequence.";

RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cytokine with immunomodulatory activity. May play a role in antiviral immunity. Up-regulates MHC class I antigen expression. Ligand for the heterodimeric class II cytokine receptor composed of IL10RB and IL28RA. The ligand/receptor complex seems to signal through the Jak-STAT pathway.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- INDUCTION: By viral infections or double stranded RNA.

CC -1- SIMILARITY: Belongs to the IL-28/IL-29 family.

CC -1- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.

CC -----

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CC -----

CC EMBL; AV129148; AAN28263.1; -; mRNA.

CC EMBL; AY184373; AAN86126.1; -; mRNA.

CC EMBL; AY336715; AAR24510.1; ALT\_INIT; mRNA.

CC Ensembl; ENSG00000183709; Homo sapiens.

CC HGNC; HGNC:18364; IL28A.

CC MIM; 607401; -.

CC Antiviral defense; Cytokine; Signal.

KW SIGNAL 1 25 Potential.

FT CHAIN 26 200 Interleukin 28A.

FT CONFLICT 151 151 T -> A (in Ref. 2).

FT SEQUENCE 200 AA; 22288 MW; DFC7B49F31BF489E CRC64;

Interferon-lambda3.  
 GN Name=IL28; Synonyms=Ifnl3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/SV;  
 RX PubMed=15120645; DOI=10.1016/j.intimp.2004.01.003;  
 RA Korten S.V., Langer J.A.;  
 RT "Full house: 12 receptors for 27 cytokines";  
 RL Int. Immunopharmacol. 4:593-608(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/SV;  
 RX PubMed=1514836; DOI=10.1099/vir.0.80904-0;  
 RA Bartlett N.W., Buttigieg K., Korten S.V., Smith G.L.;  
 RT "Murine interferon lambdas (type III interferons) exhibit potent  
 RT antiviral activity in vivo in a poxvirus infection model";  
 RL J. Gen. Virol. 86:1589-1596(2005).  
 DR EMBL; AY869696; AAX58715.1; -; mRNA.  
 DR MGI; MGI:2450574; I128.  
 SQ SEQUENCE 193 AA; 21690 MW; 9CBA23911F9B332 CRC64;  
 Query Match 48.5%; Score 463; DB 2; Length 193;  
 Best Local Similarity 58.8%; Pred. No. 3.3e-34;  
 Matches 100; Conservative 19; Mismatches 49; Indels 2; Gaps 2;  
 QY 3 PVP-TSKPTTTGKGCHGRFSLSPQELASPKKARDALLESLLKKNWSCSSPVFPNGNDL 61  
 DB 21 PVPRATRLPVEAKDCHIAQFKSLSPKELQAFKKAIAEKRLLEKDCVRCSSHLISRAWDL 80  
 QY 62 RLLQVRPVALEAEALTLTKVLEAAAGPALEDVLDQPLHLTHLSLQLOACIQPQTAG 121  
 DB 81 KQLQVQRPKALQAEVALTLKWNINDSALTTLGQPLHLTHLSLQLOCTQLQATAE 140  
 QY 122 PRPRG-RLHHLWLRLQAPKESAGCLEASVTNLFRLTLRLDLKVVADGN 170  
 DB 141 PKPPSRRLSRWLRLQEAQSKETPGCLEDVTSNLFQLLRLDLKCVASGD 190  
 RESULT 6  
 IL28\_MOUSE  
 ID IL28\_MOUSE STANDARD; PRT; 193 AA.  
 AC Q8CGK6;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Interleukin 28 precursor (interferon lambda) (IFN-lambda).  
 GN Name=IL28;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6;  
 RX PubMed=12483210; DOI=10.1038/n1875;  
 RA Korten S.V., Gallagher G., Baurin V.V., Dickensheets H., Donnelly R.P.;  
 RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;  
 RT "IFN-lambdas mediate antiviral protection through a distinct class II  
 RT cytokine receptor complex";  
 RL Nat. Immunol. 4:69-77(2003).  
 CC -!- FUNCTION: Cytokine with immunomodulatory activity. May play a role  
 CC in antiviral immunity. Up-regulates MHC class I antigen  
 CC expression. Ligand for the heterodimeric class II cytokine  
 CC receptor composed of IL10RB and IL28RA. The ligand/receptor  
 CC complex seems to signal through the Jak-STAT pathway (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- SIMILARITY: Belongs to the IL-28/IL-29 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AY184375; AAN86128.1; -; mRNA.  
 DR EMBL; ENSMUSG0000060747; Mus musculus.  
 DR MGI; MGI:2450574; I128.  
 KW Antiviral defense; Cytokine; Signal.  
 FT SIGNAL 19  
 FT CHAIN 20 193 Interleukin 28.  
 FT SEQUENCE 193 AA; 21664 MW; 357A00AACAA9BC61 CRC64;  
 Query Match 48.0%; Score 458; DB 1; Length 193;  
 Best Local Similarity 58.2%; Pred. No. 9.4e-34;  
 Matches 99; Conservative 19; Mismatches 50; Indels 2; Gaps 2;  
 QY 3 PVP-TSKPTTTGKGCHGRFSLSPQELASPKKARDALLESLLKKNWSCSSPVFPNGNDL 61  
 DB 21 PVPRATRLPVEAKDCHIAQFKSLSPKELQAFKKAIAEKRLLEKDCVRCSSHLISRAWDL 80  
 QY 62 RLLQVRPVALEAEALTLTKVLEAAAGPALEDVLDQPLHLTHLSLQLOACIQPQTAG 121  
 DB 81 KQLQVQRPKALQAEVALTLKWNINDSALTTLGQPLHLTHLSLQLOCTQLQATAE 140  
 QY 122 PRPRG-RLHHLWLRLQAPKESAGCLEASVTNLFRLTLRLDLKVVADGN 170  
 DB 141 PKPPSRRLSRWLRLQEAQSKETPGCLEDVTSNLFQLLRLDLKCVASGD 190  
 RESULT 7  
 PPK\_ACIBA  
 ID PPK\_ACIBA STANDARD; PRT; 692 AA.  
 AC Q9X4M6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Polyposphatase kinase (EC 2.7.4.1) (Polyposphoric acid kinase) (ATP-  
 DE polyposphatase phosphotransferase).  
 GN Name=ppk;  
 OS Acinetobacter baumannii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=470;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=252;  
 RX MEDLINE=20005607; PubMed=10537215;  
 RA Gavigan J.A., Marshall L.M., Dobson A.D.W.;  
 RT "Regulation of polyposphatase kinase gene expression in Acinetobacter  
 RT baumannii 252";  
 RL Microbiology 145:2931-2937(1999).  
 CC -!- FUNCTION: Catalyzes the reversible transfer of the terminal  
 CC phosphate of ATP to form a long-chain polyposphatase (polyP).  
 CC -!- CATALYTIC ACTIVITY: ATP + (phosphate)(n) = ADP + (phosphate)(n+1).  
 CC -!- PTM: An intermediate of this reaction is the autophosphorylated  
 CC ppk in which a phosphate is covalently linked to histidine  
 CC residues through a N-P bond (By similarity).  
 CC -!- SIMILARITY: Belongs to the polyposphatase kinase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AF116175; AAD28429.1; -; Genomic\_DNA.  
 DR HAWAP; MF\_00347; -; 1.  
 DR InterPro; IPR003414; PP\_kinase.  
 DR Pfam; PF02503; PP\_kinase; 1.

KW Phosphorylation; Transferase.  
FT ACT\_SITE 443 443 Phosphohistidine intermediate (By similarity).  
FT ACT\_SITE 462 462 Phosphohistidine intermediate (By similarity).  
SQ SEQUENCE 692 AA; 78980 MW; C7EB001DF332920 CRC64;  
Query Match 10.2%; Score 97.5; DB 1; Length 692;  
Best Local Similarity 22.6%; Pred. No. 4.5;  
Matches 42; Conservative 28; Mismatches 63; Indels 53; Gaps 8;  
QY 24 LSPQELAS--FKKADALEESLKXWSSCVFPGNWDRLRLQVRRVAL-----E 74  
Db 85 LSPQELHQSITAHAAERQYQILN---EQIFP-----QLREGISFLRRGELTQ 132  
QY 75 AELALTLKYLEAAGPVEDVLDQPLH-----TLHHLS-----QLQACIOPO 117  
Db 133 AQSNVWKYFQEQVAPALPTISLDAHPFPRVLVNSLNFIVLEKGDAPGQIDIAVPA 192  
QY 118 PTAGPR-----PRGRHLHWL-----HRLQAPKESAGCLEASVTFNLFLLTRD 162  
Db 193 PHSPLRVVRLPDELTEGKEHVMSSIIITHVSDSPFGWTATGCVQFRVTRNADLTIED 252  
QY 163 LKYVAD 168  
Db 253 VEDLAE 258  
RESULT 8  
Q4ZV84\_PSESY PRELIMINARY; PRT; 914 AA.  
AC Q4ZV84;  
DT 13-SEP-2005 (TremBLrel. 31, Created)  
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)  
DE SNP2-related:Helicase, C-terminal:SWIM Zn-finger.  
GN ORFNames=pfy\_1894;  
OS Pseudomonas syringae pv. syringae B728a.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=205918;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B728a;  
RG DOE Joint Genome Institute;  
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C., Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;  
RA "Comparison of two complete genome sequences of Pseudomonas syringae pv. syringae B728a and pv. tomato DC3000.";  
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B728a;  
RA Loper J.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B728a;  
RA Feil H., Fell W.S., Lindow S.E.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CP000075; AAY36938.1; -; Genomic DNA.  
DR GO; GO:0004386; F:helicase activity; IEA.  
KW Helicase.  
SQ SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5E CRC64;  
Query Match 9.4%; Score 89.5; DB 2; Length 914;  
Best Local Similarity 26.2%; Pred. No. 33;  
Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;  
QY 62 RLLOVRPRVALEALTLK-----VLEAAGPALED--VLQDPLHLHL 107  
Db 421 RLNIKAPVSLPDGLNATLRPYQLEGLSMQSLRELEVGVGLADDMGLGKTLQTLAHL 480

QY 108 SOLQACIQOPTAGPRGRHLHWLHR-----LQAPKESAGCL-EASVTEN 154  
Db 481 MEKQAGRLDRPALAVMPTSLIPNWLDESEHTPDCLKVLYGNRHRQDAGNLQDYDLILT 540  
QY 155 LFRLLTRDLK 164  
Db 541 TVALLPRDLE 550  
RESULT 9  
Q8G5G0\_BIFLO PRELIMINARY; PRT; 296 AA.  
ID Q8G5G0\_BIFLO PRELIMINARY; PRT; 296 AA.  
AC Q8G5G0;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=BL1052;  
OS Bifidobacterium longum.  
OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;  
OC Bifidobacteriaceae; Bifidobacterium.  
OX NCBI\_TaxID=216816;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=NCC 2705;  
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;  
RA Schell M.A., Kamirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwaenen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;  
RA "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
DR EMBL; AE014295; AAM24858.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 296 AA; 33881 MW; 54E29BC63276994E CRC64;  
Query Match 9.3%; Score 89; DB 2; Length 296;  
Best Local Similarity 28.9%; Pred. No. 9.8;  
Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;  
QY 46 KMW-SCSSPPFGNWDRL-LQVRRPVALEALTLKYLEAAG-----PALEDVLD 97  
Db 14 RTWRQCRTPAEPDRSVKRLILAAAHKFAQKVDVLTIRHLELGLEHTLLCVDDAID 73  
QY 98 QPLHTLHILSOACIQOPTAGPRR--GRLLHWLRLQAPKESAGCLEASVTNL 155  
Db 74 GPAQTLNRLIRKLTHPVGYR-TGAPLPRATGACRHLHLRDG-----IEHPLEFEH 124  
QY 156 FRLLTRDLKVVADGN 170  
Db 125 AR--NRD-RQVDDGD 136  
RESULT 10  
Q8DJL0\_SYNEL PRELIMINARY; PRT; 458 AA.  
ID Q8DJL0\_SYNEL PRELIMINARY; PRT; 458 AA.  
AC Q8DJL0;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
DE Isochorismate synthase.  
GN OrderedLocusNames=tll1213;  
OS Synecococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BP-1;  
RX MEDLINE=2225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,





RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.,  
 RT "Draft sequence of the Giardia lamblia genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AACB01000042; EAA40466.1; -; Genomic DNA.  
 SQ SEQUENCE 479 AA; 53677 MW; 70F50040A717818C CRC64;

Query Match 9.1%; Score 87; DB 2; Length 479;  
 Best Local Similarity 25.6%; Pred. No. 26;  
 Matches 45; Conservative 23; Mismatches 56; Indels 52; Gaps 7;

OY 11 TTGKCHIGRFXSLSPQELASPKKARDALLESK-----LKNWSSSPVPPGNWDLRLLOVRER 70  
 DB 39 TSAKIKKREKDLK-----AATYKQKEAYEQ-MKQKWSA----- 73  
 OY 71 VALEALALTLKVLAAAGPAL--EDVLDQPLHTLHHI-----LSQLQACIQPQ 117  
 DB 74 ---EALNGQLAVLEAKKESLIMTKIMEQVHLDLDDIWKTKNSLDLAQLAFQSNLKG 130  
 OY 118 PTAGPRPRGRLLHWHRLHQEAPKESAGCLESASVTNLFRLTRDLKLVADGNLSL 173  
 DB 131 ATEKANRSVLDRDAKHRLHY-LKECEGLLDAQ-----KOLEHSIIEALSIL 175

RESULT 14  
 Q5B9M4 EMENI PRELIMINARY; PRT; 967 AA.  
 AC Q5B9M4;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=AN2756.2;  
 OS Aspergillus nidulans FGSC A4.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eutiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=227321;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FGSC A4;  
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,  
 RA Boukhgelter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 RA Choepel Y., Collymore A., Cook K., Cooke P., Corum B., Dearellano K.,  
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,  
 RA Gardyna S., Gnerre S., Graham L., Grand-pierre N., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 RA Ma L.-J., Mabbitt R., McLean C., Macdonald P., Major J., Manning J.,  
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,  
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,  
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Talamas J., Teafaye S., Theodore J., Topham K., Travers M.,  
 RA Vasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander E.;  
 RT "Genome Sequence of Aspergillus nidulans."  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AACB01000049; EAA63190.1; -; Genomic DNA.  
 SQ SEQUENCE 967 AA; 109021 MW; 9BC297B7E10A1159 CRC64;

Query Match 9.1%; Score 86.5; DB 2; Length 967;  
 Best Local Similarity 25.6%; Pred. No. 67;  
 Matches 50; Conservative 28; Mismatches 62; Indels 55; Gaps 11;

OY 14 KGCHIGRFXSLSPQELASPKKARDALLESK-----LKNWSSSPVPPGNWDLRLLOVRER 68  
 DB 461 KGTEISSLLSKYNREMA-----LEALRNKTRALEEYTKNEMRNGDHELAL---RE 510  
 OY 69 RPVALEA-----ELALTLKVLAAAGPALDEDVLDQPL-HTLHLSQLQACIQPOPTAG 121  
 DB 511 KETELANQAAMDEALLEELKLSQGD--DKALDTQIDHVLHGTSTVKINDIIDSVLQGT 569  
 OY 122 PRPRGRLLHWHRLHQE-----AP-----KESAGCLESASVTNLFRLTRDLK 165  
 DB 570 VQ---RVDALYELDSTWQAGNQNASPPYVLSQEKASASATFSTAFN-----NY 617  
 OY 166 VADGNLSLRTSTHPE 180  
 DB 618 ISDG---PNSPHAE 628

RESULT 15  
 Q58D46 BOVIN PRELIMINARY; PRT; 333 AA.  
 AC Q58D46;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DE Rab geranylgeranyltransferase, alpha subunit.  
 GN Name=RABGGTA;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Pooled;  
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;  
 RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,  
 RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,  
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,  
 RA Perteau G., Holt I., Karamycheva S., Liang F., Quackenbush J.,  
 RA Keele J.W.;  
 RT "Sequence evaluation of four pooled-tissue normalized bovine CDNA  
 RL libraries and construction of a gene index for cattle."  
 RN Genome Res. 11:626-630(2001).  
 RC [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Pooled;  
 RA Harhay G.P., Sonstegard T.S., Van Tassel C.P., Clawson M.L.,  
 RA Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;  
 RT "Sequencing and analysis of Bos taurus full-length insert CDNA  
 RL clones."  
 RC Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT021751; AAX46598.1; -; mRNA.  
 DR GO; GO:0008318; F:protein prenyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0018346; P:protein amino acid prenylation; IEA.  
 KW Prenyltransferase; Repeat; Transferase.  
 SQ SEQUENCE 333 AA; 38129 MW; 4B92E0657332777A CRC64;

Query Match 9.0%; Score 86; DB 2; Length 333;  
 Best Local Similarity 27.2%; Pred. No. 21;  
 Matches 53; Conservative 18; Mismatches 54; Indels 70; Gaps 10;

OY 25 SPQELASPKAR-DALLESKLKNWSSSPVPPGNWDLR---LLQVRPVALEAL-AL 79  
 DB 81 SPEELATLVKAEGLFLESCLRV-----NPKSYGTWHHRCWLLSLPFPNWARELELCAR 134  
 OY 80 TLKV-----LEAAAGPALEDVLDQPLHTLH-----HLSQLQACIQPQ 117



```

Db      135 FLEVDERNFHCWDYRRFVAAQAAVPAEELAFDTSLITRNFSGNSWYHRSCLLLPQLHPQ 194
Qy      118 PTAGPRPRGRLL-----HHWLHLQAPAKKESAGCL-- 147
Db      195 PDSG--PQGRUPEDVLLKELELVQNAFFTDPNDQSAFYHRWL--LGRADPODARLCUHV 250
Qy      148 ---EASVTFNLFRL 159
Db      251 SRDEACLTVSFRRPL 265

```

Search completed: December 29, 2005, 13:59:11  
Job time : 230 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 29, 2005, 13:47:02 ; Search time 38 Seconds  
(without alignments)  
460.828 Million cell updates/sec  
Title: US-10-691-923-34  
Perfect score: 955  
Sequence: 1 MGPPVTSKPTTTGKGCHGR.....LKYVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	8.7	567	JC5538	Rab geranylgeranyl
2	82	8.6	899	S12319	pre-mRNA splicing
3	81.5	8.5	530	S52215	hypothetical prote
4	81.5	8.5	553	C75318	hypothetical prote
5	81.5	8.5	1086	B46335	HIV-1 retropepsin
6	80.5	8.4	468	T35928	probable aldehyde
7	80.5	8.4	1101	B45390	HIV-1 retropepsin
8	80.5	8.4	1101	GNLJVS	HIV-1 retropepsin
9	79.5	8.3	271	S27282	Bl496_F2_81 protei
10	79.5	8.3	1087	JQ1162	Poi protein - Maed
11	79	8.3	495	S270783	probable accD3 pro
12	79	8.3	557	T24538	hypothetical prote
13	78.5	8.2	253	A00251	high-affinity zinc
14	78.5	8.2	942	JC2129	protein kinase PKN
15	77.5	8.1	217	H64186	hypothetical prote
16	77.5	8.1	371	E72665	hypothetical prote
17	77.5	8.1	946	JC2130	protein kinase (EC
18	77.5	8.1	1035	A64686	cation efflux syst
19	77	8.1	775	T41961	hypothetical prote
20	77	8.1	3788	T13960	beige protein homo
21	76.5	8.0	1035	D71831	cation efflux syst
22	76	8.0	191	S57642	interferon precurs
23	76	8.0	528	C83033	benzoylformate dec
24	75.5	7.9	403	S76603	hypothetical prote
25	75.5	7.9	559	A93325	DNA repair protein
26	75.5	7.9	581	AF1923	hypothetical prote
27	75.5	7.9	649	JQ0103	hypothetical 70K p
28	75.5	7.9	654	I56134	tumor necrosis fac
29	75	7.9	640	S37869	probable serine/th

30	75	7.9	679	2	AE0694	probable membrane
31	74.5	7.8	221	2	I39198	Ram/Rab27 - human
32	74.5	7.8	268	2	S76063	hypothetical prote
33	74.5	7.8	373	2	A44478	probable cell grow
34	74.5	7.8	786	2	F70735	hypothetical prote
35	74	7.7	339	2	AI3609	daunorubicin resis
36	74	7.7	1007	2	T13693	hypothetical prote
37	73.5	7.7	189	2	JC7891	testis expressed 2
38	73.5	7.7	392	2	T43490	hypothetical prote
39	73.5	7.7	739	2	S32948	hyfp protein - Rho
40	73.5	7.7	845	2	T00071	hypothetical prote
41	73.5	7.7	1012	2	T13712	dof protein - frui
42	73.5	7.7	1144	2	T13749	dof protein - frui
43	73.5	7.7	3856	2	T51174	ataxia-telangiecta
44	73	7.6	218	2	A47285	milk fat globule p
45	73	7.6	567	2	A45977	Rab geranylgeranyl

ALIGNMENTS

RESULT 1

JC5538  
Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5538  
RiSong, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.  
Biochem. Biophys. Res. Commun. 235, 10-14, 1997  
A:Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutamina  
A:Reference number: JC5538; MUID:97339427; PMID:9196026  
A:Accession: JC5538  
A:Molecule type: DNA  
A:Residues: 1-567 <SON>  
A:Cross-references: UNIPROT:Q92696; UNIPARC:UPI000013188E  
C:Comment: This protein is involved in cutaneous disease. The gene of this enzyme is po  
C:Genetics:  
A:Gene: RabggtA  
A:Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 413  
C:Keywords: transférase

Query Match	8.7%	Score 83;	DB 2;	Length 567;
Best Local Similarity	25.6%	Pred. No. 7.9;		
Matches	50;	Conservative 16;	Mismatches 59;	Indels 70; Gaps 9;
QY	25	SQELASFKKAR-DALLESKLKWSVSPFGNWDRLQLQVRPVA-LEAELALTLK	82	
DB	81	SPEELAAVKAELGFLSCLRV-----NPKSYGTWHRCWLLGLRLPEPNWTRLELCAR	134	
QY	83	VLE-----AAAGPALEDVLDQPLHTLH-----HLSQLQACIQPQ	117	
DB	135	FLEVDERNFHCWYRRFVATQAVPPAEELAFDTSLTRNFSNYSWYRSCLLPQLHPQ	194	
QY	118	PTAGPRPRGRU-----HHWLHRLQAPKESAGCL--	147	
DB	195	PDSG--PQGRLPEDVLLKELELVQNAFTDNDQSAWPFYRWL--LGRADPDALRCLHV	250	
QY	148	---EASTFNFLRL	159	
DB	251	SRDEACLTVSFSRPL	265	

RESULT 2

S12319  
pre-mRNA splicing factor PRP6 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein YBR0508; protein YBR055C  
C:Species: Saccharomyces cerevisiae  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: S12319; S45913; S49510; S55854  
R:Legrain, P.; Choulika, A.  
EMBO J. 9, 2775-2781, 1990  
A:Title: The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cyst  
A:Reference number: S12319; MUID:90360988; PMID:2118103

Query Match	8.5%	Score 81.5;	DB 2;	Length 530;
Best Local Similarity	28.4%	Pred. No. 10;		

C;Comment: Specific enzymatic cleavages may yield mature proteins including pro  
C;Genetics:  
A;Gene: pol

A;Accession: B45390  
A:Molecule type: DNA  
A:Residues: 1-1101 <ND>  
C;Cross-references: UNIPARC:UPI0000131F26; GB:S55323; NID:g265825; PIDN:AAB25460.1; PIR:  
A;Comment: Specific enzymatic cleavages may yield mature proteins including proteinase,  
C;Genetics:  
A:Gene: pol  
C;Superfamily: pol polyprotein  
C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle  
F;35-135/Product: retropepsin #status predicted <RTP>  
F;144-856/Product: RNA-directed DNA polymerase #status predicted <REV>  
F;857-1101/Product: endonuclease #status predicted <ENC>  
F;59/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.4%; Score 80.5; DB 1; Length 1101;  
Best Local Similarity 31.6%; Pred. No. 30;  
Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;

QY 14 KGCHIGFKSLSPOLASFKKARDALRESLKL-----KNWSCSSPVF-----PGNW----D 60  
DB 155 KGPHAQW-PVTQSKLEGLKEIVDRLEKGKVGRRAPHTCNTPTFCIKCKSGKWRMLTD 213  
QY 61 LRLQLVREPRVAELAEAL 79  
DB 214 FRELNKQTEDLA-EAQGL 231

RESULT 8  
GNLJVS  
HIV-1 retropepsin (EC 3.4.23.16) - Maedi/Visna virus (strain 1514)  
C;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA pol  
N;Species: Maedi/Visna virus  
A;Date: host Homo sapiens (man)  
C;Date: 28-Feb-1986 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: A03969  
R;Sonigo, P.; Alison, M.; Staskus, K.; Klatzmamm, D.; Cole, S.; Danos, O.; Retzel, E.;  
Cell 42, 369-382, 1985  
A>Title: Nucleotide sequence of the visna lentivirus: relationship to the AIDS virus.  
A;Reference number: A90869; MUID:85254938; PMID:2410140  
A;Accession: A03969  
A:Molecule type: DNA  
A:Residues: 1-1101 <SON>  
A;Cross-references: UNIPROT:P03370; UNIPARC:UPI00001LD50A; GB:M10608  
C;Comment: Specific enzymatic cleavages may yield mature proteins including proteinase,  
C;Genetics:  
A:Gene: pol  
C;Superfamily: pol polyprotein  
C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle  
F;35-135/Product: retropepsin #status predicted <RTP>  
F;144-856/Product: RNA-directed DNA polymerase #status predicted <REV>  
F;857-1101/Product: endonuclease #status predicted <ENC>  
F;59/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.4%; Score 80.5; DB 1; Length 1101;  
Best Local Similarity 31.6%; Pred. No. 30;  
Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;

OY 14 KGCHIGFKSLSPOLASFKKARDALRESLKL-----KNWSCSSPVF-----PGNW----D 60

QY	61	LRLQVRRPVALAEAL	79
		:     :	
Db	214	FRELNKQTDLA-EAQLGL	231

RESULT 9  
S72782  
B1496 F2\_81 protein - Mycobacterium leprae  
C;Species: Mycobacterium leprae  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S72782  
R;Smith, D.R.; Robison, K.

submitted to the EMBL Data Library, November 1993  
A:Description: Mycobacterium leprae cosmid B1496.  
A:Reference number: S72695

A:Accession: S72782  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-271 <SMI>  
A:Cross-references: UNIPROT:Q49706; UNIPARC:UPI00000D4381; EMBL:U00013; NID:G466868; PID

Query Match 8.3%; Score 79.5; DB 2; Length 271;  
Best Local Similarity 26.2%; Pred. No. 6.9;  
Matches 37; Conservative 24; Mismatches 63; Indels 17; Gaps 7;  
QY 36 RDALLESKLKWSVSPVFC -NW-DLRLLQ-VREPVVALEALTLTKVLEA--AAG 89  
DB 69 KATLSLKYR-----SAPAMNGKFWLDSKVQWPDYWPVPHSTIALTVGNLSNFKTG 124  
QY 90 PALEDVLPQPLHTLHLSLOQACIQPOPTAGPRGRHLHHLHRLHLEAPKESAGCLEA 149  
DB 125 PAILGIADISNHTFTVTIDGVEA-ETPPPLPSP-----HHRPHNGEEGVMPASMGKTEF 177  
QY 150 SVTFNLFRLTLTRDLKYVADGN 170  
DB 178 PTPGKYTMVKDORSVIMDS 198

## RESULT 10

J01162  
Pol protein - Maedi/Visna virus (strain EV1)  
C:Species: Maedi/Visna virus  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: J01162  
R:Sargan, D.R.; Bennet, I.D.; Cousins, C.; Roy, D.J.; Blacklaws, B.A.; Dalziel, R.G.; W  
J. Gen. Virol. 72, 1893-1903, 1991  
A:Title: Nucleotide sequence of EV1, a British isolate of maedi-visna virus.  
A:Reference number: J01161; MUID:91341476; PMID:1651983  
A:Accession: J01162  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1087 <SAR>  
A:Cross-references: UNIPROT:Q7L206; UNIPARC:UPI00001785ED  
C:Superfamily: pol polyprotein

Query Match 8.3%; Score 79.5; DB 2; Length 1087;  
Best Local Similarity 31.6%; Pred. No. 36;  
Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;  
QY 14 KGCHGRFKSLSPQELASFKKARDALLESKL-----KNWSCSSPVF-----PGNW-----D 60  
DB 139 KGPHIAQW-PLTQEKLEGLKEIVERLEKGLGRAPPHWTNTPIFCIKKSGKWRMLID 197  
QY 61 LRLLOVRPVALEAL 79  
DB 198 FRELNKQTEDLA-EAOLGL 215

## RESULT 11

E70783  
probable accD3 protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: E70783  
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: E70783  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-495 <COL>

A:Cross-references: UNIPROT:Q10561; UNIPARC:UPI00001251BA; GB:Z73101; GB:AL123456; NID:  
A:Experimental source: strain H37RV

C:Genetics:  
A:Gene: accD3

C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 8.3%; Score 79; DB 2; Length 495;  
Best Local Similarity 28.7%; Pred. No. 16;  
Matches 35; Conservative 14; Mismatches 41; Indels 32; Gaps 5;  
QY 64 LOVRPVPVALEALTLTKVLEAAGPALEDVLPDP--LHTLHLSLOQACIQP----- 116  
DB 315 LREARRGNALAAELCLPLVLVIDAAGPALSAAAEQGLAGQIAHCLAEIVLTDTPVSTL 374  
QY 117 --QTAGP-----RPRGLHHLHRLHLEAPKESAGCLEASVTFNLFRLTLTRDLKXV 166  
DB 375 LGQSGGPGPALMPADRVLAALHGLWLP--PPEGASA-----IVFRDRTAHA 419  
QY 167 AD 168  
DB 420 AE 421

## RESULT 12

T24538  
hypothetical protein T05F1.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T24538  
R:Burton, J.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19905  
A:Accession: T24538  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-557 <WIL>  
A:Cross-references: UNIPROT:O18033; UNIPARC:UPI000007FCB7; EMBL:Z81586; PIDN:CAB04692.1  
A:Experimental source: clone T05F1  
C:Genetics:  
A:Gene: CESP:T05F1.1  
A:Map position: 1  
A:Introns: 26/3; 77/2; 119/3; 301/1; 342/2; 536/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein T05F1.1

Query Match 8.3%; Score 79; DB 2; Length 557;  
Best Local Similarity 19.9%; Pred. No. 18;  
Matches 32; Conservative 23; Mismatches 60; Indels 46; Gaps 5;  
QY 20 RFKLSLSPQELASFKKARDALLESKLKNSWSCSSPVFGNWDRLRLQVRPVALEAL 79  
DB 340 RLNSISP-----KKNIELVTKISLTVSA-----WEHEKFNKRMP-----AI 378  
QY 80 TLKVLEAAGPALEDVLPDP-----LHTLHLSLOQACIQPOPTAGP----- 123  
DB 379 TLSTLPSPDPARNISILDPALDELDINRLIGEAVLGVILDPSPGSSDSRVKSE 438  
QY 124 -----PRGLHHLHRLHLEAPKESAGCLEASVTFNL 155  
DB 439 ATMLSKDAVDKQVRVHVFIRQFASRPVGDQDRTESITSL 479

## RESULT 13

AD0251  
high-affinity zinc uptake system ATP-binding protein [imported] - Yersinia pestis (stra  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 31-Dec-2004  
C:Accession: AD0251  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B  
; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360

Qy	48	WSCSPVPFGNWDLRLLOVRP RPVALRAELAL-----TLKVLEAAGPALEDVLDQ	98
Dd	407	W----KPCGPNAPQSFTLELR---ARELELAVFWRDQGLCALRFLK-----LEDFLDN	455
Qy	99	PLHTLHILSQLQACIQPTAGPRGRLLHWHLRLHQEAPKGSAGCLEASVTF	153
Dd	456	ERH-----EVOLDMEPO-----GLVAEVTFF	476

RESULT 15  
H64186  
hypothetical protein H1159 - Haemophilus influenzae (strain Rd KW20)  
C/Species: Haemophilus influenzae  
C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C/Accession: H64186  
R/F:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; K  
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.;  
D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen,  
Science 269, 496-512, 1995  
A/Authors: Gnehm, C.B.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.  
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae  
A/Reference number: A64000; MUID:95350630; PMID:7542800

```

A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-217 <TIGR>
A;Cross-references: UNIPROT:P43786; UNIPARC:UPI000013A2D0; GB:U32795; GB:L42022

      Query Match      8.1%  Score 77.5;  DB 2;  Length 217;
      Best Local Similarity 26.2%;  Pred. No. 8.2;
      Matches 45;  Conservative 26;  Mismatches 66;  Indels 35;  Gaps 9

Qy  9  PTTTGKCHIGRPFKSLSP-QELASFKAARDALBESLKLKNWSCSSPVPPGWNWDLRLLOVR 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  27  PSVLDKSSLIQRLSIILPKBEDUKFOQALDFLQ---VENYEAAFLPLTKDAWELS--DKK 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy  68  ERPVA-LEAEALATLTKVLEAAAGPALBVDLQD-PLHLTHLHLSOLOACIQIQPTAGRP 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  81  NSDVALLYAETYYAMKKTPEA-----QEILNQIPLODRDSNHWGLOAQIELQIQAA 135
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy  126  GRLHHWHLRLOE-----APKESAGCLEASVTFNIFRLLTRDL 163
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  136  -----IQQLQADYAKNPTAEIAIKLAVQLHQAGRNEEALPL-LFGILKLTDL 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: December 29, 2005, 13:59:53  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 13:29:22 ; Search time 187 Seconds  
(without alignments)  
427.631 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGVPVTSKPTTGGKCHIGR.....LKYVADGNLSLSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq 21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	100.0	182	8	Ado59974 Met IL-28
2	955	100.0	182	9	Ady03602 Human IL-
3	951	98.6	182	9	Ady03614 Human IL-
4	950	99.5	181	8	Ado59972 IL-28A mu
5	950	99.5	181	9	Ady03600 Human IL-
6	950	99.5	182	8	Ado59978 Met IL-29
7	950	99.5	182	9	Ady03588 Human IL-
8	948	98.3	183	9	Ady03724 Human IL-
9	947	99.2	183	9	Ady03728 Human IL-
10	946	99.1	181	9	Ady03613 Human IL-
11	946	99.1	182	9	Ady03658 Human IL-
12	946	99.1	185	9	Ady03734 Human IL-
13	945	99.0	182	9	Ady03662 Human IL-
14	945	99.0	200	5	Aae18311 Human Zcy
15	945	99.0	200	5	Aae18310 Human Zcy
16	945	99.0	200	8	Ado59960 IL-29. 7/
17	945	99.0	200	9	Ady03577 Human IL-
18	944	98.8	182	9	Ady03678 Human IL-
19	941	98.5	181	9	Ady03656 Human IL-
20	941	98.5	182	9	Ady03730 Human IL-
21	941	98.5	182	9	Ady03726 Human IL-
22	940	98.4	180	9	Ady03712 Human IL-
23	940	98.4	181	9	Ady03660 Human IL-
24	940	98.4	182	9	Ady03670 Human IL-

25	940	98.4	200	5	AAU83208	Novel sec
26	940	98.4	200	5	AAE18309	Human Zcy
27	940	98.4	200	6	AAE32761	Human zcy
28	940	98.4	200	7	ADF83645	Human cyt
29	940	98.4	200	8	ADO59944	IL-29. 7/
30	940	98.4	203	5	AAE18313	Human Zcy
31	940	98.4	219	5	AAE18312	Human Zcy
32	939	98.3	181	9	ADY03676	Human IL-
33	939	98.3	182	9	ADY03650	Human IL-
34	939	98.3	182	9	ADY03686	Human IL-
35	939	98.3	200	7	ADC17329	Human IFN
36	938	98.2	200	6	AAO16278	Human IMX
37	935	97.9	181	9	ADY03668	Human IL-
38	934	97.8	181	9	ADY03648	Human IL-
39	934	97.8	181	9	ADY03684	Human IL-
40	934	97.8	182	9	ADY03654	Human IL-
41	933	97.7	179	9	ADY03714	Human IL-
42	933	97.7	182	9	ADY03666	Human IL-
43	932	97.6	182	9	ADY03682	Human IL-
44	929	97.3	178	9	ADY03716	Human IL-
45	929	97.3	181	9	ADY03652	Human IL-

#### ALIGNMENTS

RESULT 1

ADO59974

ID ADO59974 standard; protein; 182 AA.

XX

AC ADO59974;

XX

DT 29-JUL-2004 (first entry)

XX

DE Met IL-28A mutant C172S.

XX

KW interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;  
KW viral load; anti-viral antibody; serological level;  
KW alanine aminotransferase; histological improvement; hepatitis B;  
KW hepatitis C; cytopaenia; leukocyte deficiency; neutropenia;  
KW thrombocytopenia; anaemia; IL-29.

XX Homo sapiens.

XX

PH Key Location/Qualifiers

FT Misc-difference 172

FT /label= C172S

XX

PN WO2004037995-A2.

XX

PD 06-MAY-2004.

XX

PF 23-OCT-2003; 2003WO-US033628.

XX

PR 23-OCT-2002; 2002US-0420713P.

PR

23-OCT-2002; 2002US-0420714P.

PR

18-APR-2003; 2003US-0463939P.

PR

18-APR-2003; 2003US-0463982P.

XX

(ZYMO ) ZYMOGENETICS INC.

XX

PI Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KE;

XX

DR WPI; 2004-365507/34.

DR

N-PSDB; ADO59973.

XX

PT Treating hepatitis B or hepatitis C virus infection comprises  
PT administering to a mammal with a viral infection causing liver  
PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide  
PT group.

XX

PS Claim 12; SEQ ID NO 34; 102pp; English.



CC This sequence represents a mutant interleukin IL-28A, Met-C172S. This  
CC interleukin protein may be used in the method of the invention for  
CC treating a viral infection. The method comprises administering to a  
CC mammal with a viral infection causing liver inflammation, an interleukin-  
CC based polypeptide, where the viral infection level or liver inflammation  
CC is reduced. The reduction in the viral infection level is measured as a  
CC decrease in viral load, an increase in anti-viral antibodies, a decrease  
CC in serological levels of alanine aminotransferase or histological  
CC improvement. The viral infection is hepatitis B or C virus infection. The  
CC mammal has cytopaenia, comprising leukocyte deficiency, neutropenia,  
CC thrombocytopenia or anaemia. The interleukin polypeptide is useful in  
CC 28 or 29, or a variant of these. The method of the invention is useful in  
CC treating hepatitis B or C virus infection.

XX Sequence 182 AA;

Query Match 100.0%; Score 955; DB 8; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.8e-91;  
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWSCSPVPFGNWD 60  
Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWSCSPVPFGNWD 60  
Qy 61 LRLQLVRRPVALEAELALTLKYLEAAAGPALEDVLDQPLHTLHILSLOLQACIQPPTA 120  
Db 61 LRLQLVRRPVALEAELALTLKYLEAAAGPALEDVLDQPLHTLHILSLOLQACIQPPTA 120  
Qy 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLTDLKYVADGNLSLRTSTHPE 180  
Db 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLTDLKYVADGNLSLRTSTHPE 180  
Qy 181 ST 182  
Db 181 ST 182

RESULT 2

ADY03602  
ID ADY03602 standard; protein; 182 AA.

XX AC ADY03602;

XX 05-MAY-2005 (first entry)

XX Human IL-29 mutant protein sequence SeqID29.

XX antiviral; pharmaceutical; hepatitis b virus infection;

KW hepatitis c virus infection; mutant; mutein; IL-29.

XX Homo sapiens.

OS Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

XX 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

XX (BRAD//) BRADY L J.

PA (KLUC//) KLUCHER K M.

PA (CHAN//) CHAN C.

PA (DONG//) DONG D L.

PA (LIUH//) LIU H Y.

PA (SHEP//) SHEPPARD P O.

PA (BUKO//) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;

PI Bukowski TR;

XX WPI; 2005-180368/19.  
DR N-PSDB; ADY03601.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-  
PT viral activity, useful for treating hepatitis B or hepatitis C  
PT infections.

XX Claim 1; SEQ ID NO 29; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29  
CC polypeptide having antiviral activity. One or more of the cysteine  
CC residues were mutated to produce the proteins of the invention. The  
CC invention may be useful for the development of a pharmaceutical  
CC composition for the treatment of hepatitis B or C. The present sequence  
CC is that of a novel IL variant protein of the invention.

XX Sequence 182 AA;

Query Match 100.0%; Score 955; DB 9; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.8e-91;  
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWSCSPVPFGNWD 60  
Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWSCSPVPFGNWD 60  
Qy 61 LRLQLVRRPVALEAELALTLKYLEAAAGPALEDVLDQPLHTLHILSLOLQACIQPPTA 120  
Db 61 LRLQLVRRPVALEAELALTLKYLEAAAGPALEDVLDQPLHTLHILSLOLQACIQPPTA 120  
Qy 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLTDLKYVADGNLSLRTSTHPE 180  
Db 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLTDLKYVADGNLSLRTSTHPE 180  
Qy 181 ST 182  
Db 181 ST 182

RESULT 3

ADY03614

ID ADY03614 standard; protein; 182 AA.

XX AC ADY03614;

XX 05-MAY-2005 (first entry)

XX Human IL-28A mutant protein sequence SeqID41.

XX antiviral; pharmaceutical; hepatitis b virus infection;

KW hepatitis c virus infection; mutant; mutein; IL-28A.

XX Homo sapiens.

OS Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

XX 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

XX (BRAD//) BRADY L J.

PA (KLUC//) KLUCHER K M.

PA (CHAN//) CHAN C.

PA (DONG//) DONG D L.

PA (LIUH//) LIU H Y.

PA (SHEP//) SHEPPARD P O.

PA (BUKO//) BUKOWSKI T R.

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XX PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI Bukowski TR;
XX WPI; 2005-180368/19.
DR N-PSDB; ADY03608.
XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
PT viral activity, useful for treating hepatitis B or hepatitis C
PT infections.
XX Claim 1; SEQ ID NO 41; 149pp; English.
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
CC polypeptide having antiviral activity. One or more of the cysteine
CC residues were mutated to produce the proteins of the invention. The
CC invention may be useful for the development of a pharmaceutical
CC composition for the treatment of hepatitis B or C. The present sequence
CC is that of a novel IL variant protein of the invention.
XX SQ Sequence 182 AA;
Query Match 99.6%; Score 951; DB 9; Length 182;
Best Local Similarity 99.5%; Pred. No. 7.3e-91;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGVPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
DB 1 MGVPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
QY 61 LRLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPPTA 120
DB 61 LRLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPPTA 120
QY 121 GPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180
DB 121 GPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180
QY 181 ST 182
DB 181 ST 182
RESULT 4
AD059972
ID AD059972 standard; protein; 181 AA.
XX AC
XX AD059972;
DT 29-JUL-2004 (first entry)
DE IL-28A mutant C171S.
XX interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;
KW viral load; anti-viral antibody; serological level;
KW alanine aminotransferase; histological improvement; hepatitis B;
KW hepatitis C; cytopenia; leukocyte deficiency; neutropenia;
KW thrombocytopenia; anaemia; IL-29.
XX OS
XX Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 171 /label= C171S
FT
XX WO2004037995-A2.
XX 06-MAY-2004.
XX 23-OCT-2003; 2003WO-US033628.
XX 23-OCT-2002; 2002US-0420713P.
XX 23-OCT-2002; 2002US-0420714P.
XX PD
XX PR
```

```
PR 18-APR-2003; 2003US-0463939P.
PR 18-APR-2003; 2003US-0463982P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KE;
XX WPI; 2004-365507/34.
DR N-PSDB; AD059971.
XX Treating hepatitis B or hepatitis C virus infection comprises
PT administering to a mammal with a viral infection causing liver
PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide
PT group.
XX Claim 12; SEQ ID NO 32; 102pp; English.
XX This sequence represents a mutant interleukin IL-28A, Met-C171S. This
CC interleukin protein may be used in the method of the invention for
CC treating a viral infection. The method comprises administering to a
CC mammal with a viral infection causing liver inflammation, an interleukin-
CC based polypeptide, where the viral infection level or liver inflammation
CC is reduced. The reduction in the viral infection level is measured as a
CC decrease in viral load, an increase in anti-viral antibodies, a decrease
CC in serological levels of alanine aminotransferase or histological
CC improvement. The viral infection is hepatitis B or C virus infection. The
CC mammal has cytopenia, comprising leukocyte deficiency, neutropenia,
CC thrombocytopenia or anaemia. The interleukin polypeptide is interleukin
CC 28 or 29, or a variant of these. The method of the invention is useful in
CC treating hepatitis B or C virus infection.
XX SQ Sequence 181 AA;
Query Match 99.5%; Score 950; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 9.2e-91;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPVPTSKEPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 61
DB 1 GPVTSKEPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
QY 62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPPTAG 121
DB 61 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPPTAG 120
QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPS 181
DB 121 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPS 180
QY 182 T 182
DB 181 T 181
RESULT 5
ADY03600
ID ADY03600 standard; protein; 181 AA.
XX AC
XX ADY03600;
XX 05-MAY-2005 (first entry)
XX Human IL-29 mutant protein sequence SeqID27.
XX antiviral; pharmaceutical; hepatitis b virus infection;
KW hepatitis c virus infection; mutant; mutein; IL-29.
XX OS
XX Homo sapiens.
XX Synthetic.
XX US2005037012-A1.
XX 17-FEB-2005.
```

```

XX 09-AUG-2004; 2004US-00914772.
XX PF
XX 07-AUG-2003; 2003US-0493194P.
XX PR
XX 10-MAR-2004; 2004US-0551841P.
XX PR
XX 02-APR-2004; 2004US-0559142P.
XX PR
XX (BRAD//) BRADY L J.
XX PA
XX (KLUC//) KLUCHER K M.
XX PA
XX (CHAN//) CHAN C.
XX PA
XX (DONG//) DONG D L.
XX PA
XX (LIUH//) LIU H Y.
XX PA
XX (SHEP//) SHEPPARD P O.
XX PA
XX (BUKO//) BUKOWSKI T R.
XX PA
XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
XX PI Bukowski TR;
XX PI
XX WPI; 2005-180368/19.
XX DR
XX N-PSDB; ADY03599.
XX DR
XX Novel isolated interleukin-28A, IL-28B or IL-29 polypeptide having anti-
XX PT viral activity, useful for treating hepatitis B or hepatitis C
XX PT infections.
XX PT
XX Claim 1; SEQ ID NO 27; 149pp; English.
XX PS
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
XX CC polypeptide having antiviral activity. One or more of the cysteine
XX CC residues were mutated to produce the proteins of the invention. The
XX CC invention may be useful for the development of a pharmaceutical
XX CC composition for the treatment of hepatitis B or C. The present sequence
XX CC is that of a novel IL variant protein of the invention.
XX CC
XX Sequence 181 AA;
XX SQ
Query Match 99.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 9.2e-91;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 61
Db 1 GPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 60
Qy 62 RLLOVRERPVVALEALALTILKYLEAAGPALEDVLDQPLHTLHLLHLSQLQACIQOPTAG 121
Db 61 RLLOVRERPVVALEALALTILKYLEAAGPALEDVLDQPLHTLHLLHLSQLQACIQOPTAG 120
Qy 122 PRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLITRDLKYVADGNLSLRTSTHPES 181
Db 121 PRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLITRDLKYVADGNLSLRTSTHPES 180
Qy 182 T 182
Db 181 T 181
RESULT 6
AD059978
ID AD059978 standard; protein; 182 AA.
XX AC
XX AD059978;
XX AC
XX 29-JUL-2004 (first entry)
XX DT
XX Met IL-29.
XX DE
XX interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;
XX KW viral load; anti-viral antibody; serological level;
XX KW alanine aminotransferase; histological improvement; hepatitis B;
XX KW hepatitis C; cytopaenia; leukocyte deficiency; neutropenia;
XX KW thrombocytopenia; anaemia; IL-29.
XX KW

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OS Homo sapiens.
XX PN
XX WO2004037995-A2.
XX PD
XX 06-MAY-2004.
XX PF
XX 23-OCT-2003; 2003WO-US033628.
XX PR
XX 23-OCT-2002; 2002US-0420713P.
XX PR
XX 23-OCT-2002; 2002US-0420714P.
XX PR
XX 18-APR-2003; 2003US-0463939P.
XX PR
XX 18-APR-2003; 2003US-0463982P.
XX XX
XX (ZYMO ) ZYMOGENETICS INC.
XX XX
XX Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KE;
XX PI
XX WPI; 2004-365507/34.
XX DR
XX N-PSDB; ADOS9977.
XX DR
XX Treating hepatitis B or hepatitis C virus infection comprises
XX PT administering to a mammal with a viral infection causing liver
XX PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide
XX PT group.
XX XX
XX Claim 13; SEQ ID NO 38; 102pp; English.
XX PS
XX This sequence represents an interleukin Met-IL-29. This interleukin
XX CC protein may be used in the method of the invention for treating a viral
XX CC infection. The method comprises administering to a mammal with a viral
XX CC infection causing liver inflammation, an interleukin-based polypeptide,
XX CC where the viral infection level or liver inflammation is reduced. The
XX CC reduction in the viral infection level is measured as a decrease in viral
XX CC load, an increase in anti-viral antibodies, a decrease in serological
XX CC levels of alanine aminotransferase or histological improvement. The viral
XX CC infection is hepatitis B or C virus infection. The mammal has cytopaenia,
XX CC comprising leukocyte deficiency, neutropenia, thrombocytopenia or
XX CC anaemia. The interleukin polypeptide is interleukin 28 or 29, or a
XX CC variant of these. The method of the invention is useful in treating
XX CC hepatitis B or C virus infection.
XX XX
XX Sequence 182 AA;
XX SQ
Query Match 99.5%; Score 950; DB 8; Length 182;
Best Local Similarity 99.5%; Pred. No. 9.3e-91;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 60
Db 1 MGPVTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 60
Qy 61 LRLLOVRERPVVALEALALTILKYLEAAGPALEDVLDQPLHTLHLLHLSQLQACIQOPTA 120
Db 61 LRLLOVRERPVVALEALALTILKYLEAAGPALEDVLDQPLHTLHLLHLSQLQACIQOPTA 120
Qy 121 GPRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLITRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLITRDLKYVADGNLSLRTSTHPE 180
Qy 181 ST 182
Db 181 ST 182
RESULT 7
ADY03588
ID ADY03588 standard; protein; 182 AA.
XX AC
XX ADY03588;
XX AC
XX 05-MAY-2005 (first entry)
XX DT
XX Human IL-29 mutant protein sequence SeqID15.
XX DE

```

XX antiviral; pharmaceutical; hepatitis b virus infection;  
 KW hepatitis c virus infection; mutant; mutein; IL-29.  
 XX  
 OS Homo sapiens.  
 XX Synthetic.  
 XX US2005037012-A1.  
 XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.  
 XX 07-AUG-2003; 2003US-0493194P.  
 PR 10-MAR-2004; 2004US-0551841P.  
 PR 02-APR-2004; 2004US-0559142P.  
 XX

PA (BRAD/) BRADY L J.  
 PA (KLUC/) KLUCHER K M.  
 PA (CHAN/) CHAN C.  
 PA (DONG/) DONG D L.  
 PA (LIUH/) LIU H Y.  
 PA (SHEP/) SHEPPARD P O.  
 PA (BUKO/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;  
 PI Bukowski TR;  
 XX

XX WPI; 2005-180368/19.  
 DR N-PSDB; ADY03587.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-  
 PT viral activity, useful for treating hepatitis B or hepatitis C  
 PT infections.

XX Example 19; SEQ ID NO 15; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29  
 CC polypeptide having antiviral activity. One or more of the cysteine  
 CC residues were mutated to produce the proteins of the invention. The  
 CC invention may be useful for the development of a pharmaceutical  
 CC composition for the treatment of hepatitis B or C. The present sequence  
 CC is that of a novel IL variant protein of the invention.

XX Sequence 182-AA;

Query Match 99.5%; Score 950; DB 9; Length 182;  
 Best Local Similarity 99.5%; Pred. No. 9.3e-91;  
 Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSSPVFPGNWD 60  
 DB 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSSPVFPGNWD 60  
 QY 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120  
 DB 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120  
 QY 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180  
 DB 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180  
 QY 181 ST 182  
 DB 181 ST 182

RESULT 8  
 ADY03724  
 ID ADY03724 standard; protein; 183 AA.  
 XX  
 AC ADY03724;  
 XX

DT 05-MAY-2005 (first entry)

XX Human IL-29 mutant protein sequence SeqID151.

XX antiviral; pharmaceutical; hepatitis b virus infection;  
 KW hepatitis c virus infection; mutant; mutein; IL-29.  
 XX

OS Homo sapiens.  
 XX Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

PR 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

PA (BRAD/) BRADY L J.

PA (KLUC/) KLUCHER K M.

PA (CHAN/) CHAN C.

PA (DONG/) DONG D L.

PA (LIUH/) LIU H Y.

PA (SHEP/) SHEPPARD P O.

PA (BUKO/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;  
 PI Bukowski TR;  
 XX

XX WPI; 2005-180368/19.

DR N-PSDB; ADY03723.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-  
 PT viral activity, useful for treating hepatitis B or hepatitis C  
 PT infections.

XX Claim 1; SEQ ID NO 151; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29  
 CC polypeptide having antiviral activity. One or more of the cysteine  
 CC residues were mutated to produce the proteins of the invention. The  
 CC invention may be useful for the development of a pharmaceutical  
 CC composition for the treatment of hepatitis B or C. The present sequence  
 CC is that of a novel IL variant protein of the invention.

XX Sequence 183 AA;

Query Match 99.3%; Score 948; DB 9; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 1.5e-90;  
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSSPVFPGNWD 60  
 DB 2 LGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSSPVFPGNWD 61  
 QY 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120  
 DB 62 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 121  
 QY 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180  
 DB 122 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 181  
 QY 181 ST 182  
 DB 182 ST 183

RESULT 9  
 ADY03728  
 ID ADY03728 standard; protein; 183 AA.

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XX ADY03728;
AC
XX 05-MAY-2005 (first entry)
DT
XX Human IL-29 mutant protein sequence SeqID155.
DE
XX antiviral; pharmaceutical; hepatitis b virus infection;
KW hepatitis c virus infection; mutant; mutein; IL-29.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005037012-A1.
XX
PD 17-FEB-2005.
XX
XX 09-AUG-2004; 2004US-00914772.
PF
XX 07-AUG-2003; 2003US-0493194P.
PR
XX 10-MAR-2004; 2004US-0551841P.
PR
XX 02-APR-2004; 2004US-0559142P.
XX
XX (BRAD/) BRADY L J.
PA (KLUC/) KLUCHER K M.
PA (CHAN/) CHAN C.
PA (DONG/) DONG D L.
PA (LIUH/) LIU H Y.
PA (SHEP/) SHEPPARD P O.
PA (BUKO/) BUKOWSKI T R.
XX
XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI Bukowski TR;
PI
XX WPI; 2005-180368/19.
DR N-PSDB; ADY03727.
XX
XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
PT viral activity, useful for treating hepatitis B or hepatitis C
PT infections.
XX
XX Claim 1; SEQ ID NO 155; 149pp; English.
XX
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
CC polypeptide having antiviral activity. One or more of the cysteine
CC residues were mutated to produce the proteins of the invention. The
CC invention may be useful for the development of a pharmaceutical
CC composition for the treatment of hepatitis B or C. The present sequence
CC is that of a novel IL variant protein of the invention.
XX
XX Sequence 183 AA;
XX
Query Match 99.2%; Score 947; DB 9; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.9e-90;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGPVPTSKPTTGGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPGNWD 60
DB 2 IGVPTSKPTTGGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPGNWD 61
QY 61 LRLQVRRPVALEAELALTAKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 120
DB 62 LRLQVRRPVALEAELALTAKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 121
QY 121 GPRPGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 180
DB 122 GPRPGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 181
QY 181 ST 182
DB 182 ST 183

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RESULT 10
ADY03613
ID ADY03613 standard; protein; 181 AA.
XX
XX AC ADY03613;
XX
XX 05-MAY-2005 (first entry)
DT
XX Human IL-28A mutant protein sequence SeqID40.
DE
XX antiviral; pharmaceutical; hepatitis b virus infection;
KW hepatitis c virus infection; mutant; mutein; IL-28A.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005037012-A1.
XX
PD 17-FEB-2005.
XX
XX 09-AUG-2004; 2004US-00914772.
PF
XX 07-AUG-2003; 2003US-0493194P.
PR
XX 10-MAR-2004; 2004US-0551841P.
PR
XX 02-APR-2004; 2004US-0559142P.
XX
XX (BRAD/) BRADY L J.
PA (KLUC/) KLUCHER K M.
PA (CHAN/) CHAN C.
PA (DONG/) DONG D L.
PA (LIUH/) LIU H Y.
PA (SHEP/) SHEPPARD P O.
PA (BUKO/) BUKOWSKI T R.
XX
XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI Bukowski TR;
PI
XX WPI; 2005-180368/19.
DR N-PSDB; ADY03607.
XX
XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
PT viral activity, useful for treating hepatitis B or hepatitis C
PT infections.
XX
XX Claim 1; SEQ ID NO 40; 149pp; English.
XX
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
CC polypeptide having antiviral activity. One or more of the cysteine
CC residues were mutated to produce the proteins of the invention. The
CC invention may be useful for the development of a pharmaceutical
CC composition for the treatment of hepatitis B or C. The present sequence
CC is that of a novel IL variant protein of the invention.
XX
XX Sequence 181 AA;
XX
Query Match 99.1%; Score 946; DB 9; Length 181;
Best Local Similarity 99.4%; Pred. No. 2.4e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPVPTSKPTTGGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPGNWD 61
DB 1 GPVPTSKPTTGGKCHIGRFKSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPGNWD 60
QY 62 LRLQVRRPVALEAELALTAKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 121
DB 61 LRLQVRRPVALEAELALTAKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 120
QY 122 PRPGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 181
DB 121 PRPGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 180
QY 182 T 182

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Db      181 T 181
RESULT 11
ADY03658
ID      ADY03658 standard; protein; 182 AA.
XX
AC      ADY03658;
XX
DT      05-MAY-2005 (first entry)
XX
DE      Human IL-29 mutant protein sequence SeqID85.
XX
KW      antiviral; pharmaceutical; hepatitis b virus infection;
KW      hepatitis c virus infection; mutant; mutein; IL-29.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FN      US2005037012-A1.
XX
PD      17-FEB-2005.
XX
PF      09-AUG-2004; 2004US-00914772.
XX
PR      07-AUG-2003; 2003US-0493194P.
PR      10-MAR-2004; 2004US-0551841P.
PR      02-APR-2004; 2004US-0559142P.
XX
PA      (BRAD//) BRADY L J.
PA      (KLUC//) KLUCHER K M.
PA      (CHAN//) CHAN C.
PA      (DONG//) DONG D L.
PA      (LIUH//) LIU H Y.
PA      (SHEP//) SHEPPARD P O.
PA      (BUKO//) BUKOWSKI T R.
XX
PI      Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI      Bukowski TR;
XX
WPI; 2005-180368/19.
DR      N-PSDB; ADY03657.
XX
PT      Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
PT      viral activity, useful for treating hepatitis B or hepatitis C
PT      infections.
XX
PS      Claim 1; SEQ ID NO 85; 149pp; English.
XX
CC      This invention relates to a novel isolated IL-28A, IL-28B or IL-29
CC      polypeptide having antiviral activity. One or more of the cysteine
CC      residues were mutated to produce the proteins of the invention. The
CC      invention may be useful for the development of a pharmaceutical
CC      composition for the treatment of hepatitis B or C. The present sequence
CC      is that of a novel IL variant protein of the invention.
XX
SQ      Sequence 182 AA;
Query Match      99.1%; Score 946; DB 9; Length 182;
Best Local Similarity 98.9%; Pred. No. 2.4e-90;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 MGVPVTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 60
Db      1 MGVPVTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 60
Qy      61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
Db      61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
Qy      121 GPRPRGLHHLHRLQEPKESAGCLESVTFNLFRLTLTRDLKYVADGNLSLTSTHPE 180
Db      121 GPRPRGLHHLHRLQEPKESAGCLESVTFNLFRLTLTRDLKYVADGNLSLTSTHPE 180

Qy      181 ST 182
Db      181 ST 182
RESULT 12
ADY03734
ID      ADY03734 standard; protein; 185 AA.
XX
AC      ADY03734;
XX
DT      05-MAY-2005 (first entry)
XX
DE      Human IL-29 mutant protein sequence SeqID161.
XX
KW      antiviral; pharmaceutical; hepatitis b virus infection;
KW      hepatitis c virus infection; mutant; mutein; IL-29.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FN      US2005037012-A1.
XX
PD      17-FEB-2005.
XX
PF      09-AUG-2004; 2004US-00914772.
XX
PR      07-AUG-2003; 2003US-0493194P.
PR      10-MAR-2004; 2004US-0551841P.
PR      02-APR-2004; 2004US-0559142P.
XX
PA      (BRAD//) BRADY L J.
PA      (KLUC//) KLUCHER K M.
PA      (CHAN//) CHAN C.
PA      (DONG//) DONG D L.
PA      (LIUH//) LIU H Y.
PA      (SHEP//) SHEPPARD P O.
PA      (BUKO//) BUKOWSKI T R.
XX
PI      Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI      Bukowski TR;
XX
WPI; 2005-180368/19.
DR      N-PSDB; ADY03733.
XX
PT      Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
PT      viral activity, useful for treating hepatitis B or hepatitis C
PT      infections.
XX
PS      Claim 1; SEQ ID NO 161; 149pp; English.
XX
CC      This invention relates to a novel isolated IL-28A, IL-28B or IL-29
CC      polypeptide having antiviral activity. One or more of the cysteine
CC      residues were mutated to produce the proteins of the invention. The
CC      invention may be useful for the development of a pharmaceutical
CC      composition for the treatment of hepatitis B or C. The present sequence
CC      is that of a novel IL variant protein of the invention.
XX
SQ      Sequence 185 AA;
Query Match      99.1%; Score 946; DB 9; Length 185;
Best Local Similarity 99.4%; Pred. No. 2.5e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      5 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 64
Qy      62 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      65 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 124
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QY 122 PRPRGRHLHRLHRLQAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 181  
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 DB 125 PRPRGRHLHRLHRLQAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 184  
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 QY 182 T 182  
 ||  
 DB 185 T 185

RESULT 13  
 ADY03662  
 ID ADY03662 standard; protein; 182 AA.  
 XX  
 AC ADY03662;  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Human IL-29 mutant protein sequence SeqID89.  
 XX  
 KW antiviral; pharmaceutical; hepatitis b virus infection;  
 KW hepatitis c virus infection; mutant; mutein; IL-29.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US2005037012-A1.  
 XX  
 PD 17-FEB-2005.  
 XX  
 PF 09-AUG-2004; 2004US-00914772.  
 XX  
 PR 07-AUG-2003; 2003US-0493194P.  
 PR 10-MAR-2004; 2004US-0551841P.  
 PR 02-APR-2004; 2004US-0559142P.  
 XX  
 PA (BRAD//) BRADY L J.  
 PA (KLUC//) KLUCHER K M.  
 PA (CHAN//) CHAN C.  
 PA (DONG//) DONG D L.  
 PA (LIUH//) LIU H Y.  
 PA (SHEP//) SHEPPARD P O.  
 PA (BUKO//) BUKOWSKI T R.  
 XX  
 PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;  
 PI Bukowski TR;  
 PI  
 DR WPI; 2005-180368/19.  
 DR N-PSDB; ADY03661.  
 XX  
 PT Novel isolated interleukin-28A, IL-28B or IL-29 polypeptide having anti-  
 PT viral activity, useful for treating hepatitis B or hepatitis C  
 PT infections.  
 XX  
 PS Claim 1; SEQ ID NO 89; 149pp; English.  
 XX  
 CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29  
 CC polypeptide having antiviral activity. One or more of the cysteine  
 CC residues were mutated to produce the proteins of the invention. The  
 CC invention may be useful for the development of a pharmaceutical  
 CC composition for the treatment of hepatitis B or C. The present sequence  
 CC is that of a novel IL variant protein of the invention.  
 XX  
 SQ Sequence 182 AA;  
 Query Match 99.0%; Score 945; DB 9; Length 182;  
 Best Local Similarity 98.9%; Pred. NO. 3.1e-90;  
 Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MGPVPTSKPTTGKCHIGRFKSLSPQELASFKKARDALERSLKLNWCSPPVPPGNWD 60  
 |||||  
 DB 1 MGPVPTSKPTTGKCHIGRFKSLSPQELASFKKARDALERSLKLNWCSPPVPPGNWD 60  
 |||||  
 QY 61 LRLQVRRPVALEALTLKVLAAAGPALEDVLDOPHLTHLHLSQLQACIQPQPTA 120  
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DB 61 LRLQVRRPVALEALTLKVLAAAGPALEDVLDOPHLTHLHLSQLQACIQPQPTA 120  
 |||||  
 QY 121 GPRPRGRHLHRLHRLQAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180  
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 DB 121 GPRPRGRHLHRLHRLQAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180  
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 QY 181 ST 182  
 ||  
 DB 181 ST 182

RESULT 14  
 AAE18311  
 ID AAE18311 standard; protein; 200 AA.  
 XX  
 AC AAE18311;  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Human Zcyto21 consensus protein.  
 XX  
 KW Human; interferon like protein; IFN; genetic disease; transgenic animal;  
 KW cancer; immune regulation; rheumatoid arthritis; multiple sclerosis;  
 KW myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation;  
 KW tumour; viral infection; graft rejection; human immuno deficiency virus;  
 KW HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;  
 KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive;  
 KW Zcyto21 protein; chromosome 19q13.13.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202627-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US021087.  
 XX  
 PR 30-JUN-2000; 2000US-0215446P.  
 PR 20-APR-2001; 2001US-0285424P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Sheppard PO, Presnell SR, Fox BA, Gilbert T, Haldeman BA;  
 PI Grant FJ;  
 PI  
 DR WPI; 2002-171640/22.  
 DR N-PSDB; AAD29146.  
 XX  
 PT New polypeptide Zcyto21, which is related to interferon, is useful e.g.  
 PT for treating viral infection and immunological disease.  
 XX  
 PS Disclosure; Page 75; 82pp; English.  
 XX  
 CC The patent discloses novel polynucleotide and polypeptide molecules for  
 CC Zcyto21, an interferon (IFN) like protein which is most closely related  
 CC to INF-alpha. Zcyto21 DNAs are useful for detecting the corresponding  
 CC genes and its mutants, e.g. for diagnosis of genetic diseases and cancer  
 CC or for detecting chromosome 19 deletions and translocations associated  
 CC with diseases. They are useful for preparing transgenic animals used to  
 CC study the Zcyto21 gene and protein and as antisense inhibitors. Zcyto21  
 CC sequences and their inhibitors are useful for treating diseases that  
 CC require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis,  
 CC myasthenia gravis, systemic lupus erythematosus and diabetes), tumours,  
 CC inflammation (e.g. arthritis or sepsis), viral infections (e.g. human  
 CC immune deficiency viruses (HIV) and papilloma viruses), graft rejection,  
 CC behavioural and reproductive disorders. They are also used as vaccine  
 CC adjuvants. They can also be used to identify specific inhibitors and  
 CC receptors. The present sequence is human Zcyto21 consensus protein.  
 CC Zcyto21 gene is located on chromosome 19q13.13  
 XX  
 SQ Sequence 200 AA;



Query Match 99.0%; Score 945; DB 5; Length 200;  
Best Local Similarity 99.4%; Pred. No. 3.5e-90;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 61  
DB 20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 79

QY 62 RLQVRERPVVALEAELALTLKVEAAGPALEDVLDQPLHTLHHLSQLOACIQOPTAG 121  
DB 80 RLQVRERPVVALEAELALTLKVEAAGPALEDVLDQPLHTLHHLSQLOACIQOPTAG 139

QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPES 181  
DB 140 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPES 199

QY 182 T 182  
DB 200 T 200

RESULT 15  
AAE18310  
ID AAE18310 standard; protein; 200 AA.  
XX  
AC AAE18310;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Human Zcyto21 allelic variant protein.  
XX  
KW Human; interferon like protein; IFN; genetic disease; transgenic animal;  
KW cancer; immune regulation; rheumatoid arthritis; multiple sclerosis;  
KW myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation;  
KW tumour; viral infection; graft rejection; human immuno deficiency virus;  
KW HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;  
KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive;  
KW Zcyto21 protein.  
XX  
OS Homo sapiens.  
XX  
PN WO200202627-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US021087.  
XX  
PR 30-JUN-2000; 2000US-0215446P.  
PR 20-APR-2001; 2001US-0285424P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sheppard PO, Presnell SR, Fox BA, Gilbert T, Haldeman BA;  
PI Grant PJ;  
XX  
DR WPI; 2002-171640/22.  
DR N-PSDB; AAD29145.  
XX  
PT New polypeptide Zcyto21, which is related to interferon, is useful e.g.  
PT for treating viral infection and immunological disease.  
XX  
PS Disclosure; Page 72-73; 82pp; English.  
XX

CC inflammation (e.g. arthritis or sepsis), viral infections (e.g., human  
CC immune deficiency viruses (HIV) and papilloma viruses), graft rejection,  
CC behavioural and reproductive disorders. They are also used as vaccine  
CC adjuvants. The present sequence is human Zcyto21 allelic variant protein  
CC receptors. The present sequence is human Zcyto21 allelic variant protein  
XX  
SQ Sequence 200 AA;

Query Match 99.0%; Score 945; DB 5; Length 200;  
Best Local Similarity 99.4%; Pred. No. 3.5e-90;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 61  
DB 20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 79

QY 62 RLQVRERPVVALEAELALTLKVEAAGPALEDVLDQPLHTLHHLSQLOACIQOPTAG 121  
DB 80 RLQVRERPVVALEAELALTLKVEAAGPALEDVLDQPLHTLHHLSQLOACIQOPTAG 139

QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPES 181  
DB 140 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPES 199

QY 182 T 182  
DB 200 T 200

Search completed: December 29, 2005, 13:55:15  
Job time : 188 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 29, 2005, 13:47:27 ; Search time 46 Seconds  
(without alignments)  
327.108 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPVTSKPTTGGCHIGR.....LKYVADGNLSLRTSTHPST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	99.0	200	2	US-09-895-834-5
2	945	99.0	200	2	US-09-895-834-7
3	940	98.4	200	2	US-09-893-737-268
4	940	98.4	200	2	US-09-895-834-2
5	940	98.4	203	2	US-09-895-834-12
6	940	98.4	219	2	US-09-895-834-9
7	83	8.7	567	2	US-09-538-092-1365
8	82	8.6	315	2	US-09-370-398-6
9	82	8.6	315	2	US-10-090-190-6
10	82	8.6	315	2	US-10-082-902-6
11	82	8.6	899	2	US-09-538-092-27
12	81.5	8.5	1228	2	US-09-252-991A-17764
13	81	8.5	164	2	US-10-104-047-3099
14	80	8.4	563	1	PCT-US94-05268-2
15	80	8.4	563	4	PCT-US94-05268-2
16	79.5	8.3	315	2	US-08-965-9038-8
17	79.5	8.3	315	2	US-09-370-398-3
18	79.5	8.3	315	2	US-10-090-190-3
19	79.5	8.3	315	2	US-10-082-902-3
20	79	8.3	495	2	US-09-712-363-181
21	79	8.3	903	2	US-09-758-007-1
22	79	8.3	1114	2	US-09-637-145-4
23	78.5	8.2	378	2	US-09-724-797-40
24	78.5	8.2	780	2	US-09-771-161A-144
25	78.5	8.2	942	2	US-08-685-852-3
26	78.5	8.2	942	2	US-09-771-161A-235
27	78.5	8.2	942	2	US-09-771-161A-236

28	77.5	8.1	180	2	US-09-252-991A-18500	Sequence 18500, A
29	77	8.1	198	2	US-09-489-039A-9420	Sequence 9420, Ap
30	77	8.1	542	2	US-09-252-991A-32139	Sequence 32139, A
31	76	8.0	302	2	US-09-489-039A-7999	Sequence 7999, Ap
32	76	8.0	560	2	US-09-252-991A-27301	Sequence 27301, A
33	75.5	7.9	654	2	US-09-949-002-389	Sequence 389, App
34	75.5	7.9	683	2	US-09-949-002-424	Sequence 424, App
35	75	7.9	229	2	US-09-270-767-31836	Sequence 31836, A
36	75	7.9	640	2	US-09-487-558B-84	Sequence 94, Appl
37	74.5	7.8	227	2	US-09-949-016-10420	Sequence 10420, A
38	74.5	7.8	373	2	US-09-919-497-53	Sequence 53, Appl
39	74.5	7.8	384	2	US-09-949-016-11663	Sequence 11663, A
40	74.5	7.8	767	2	US-09-949-016-6167	Sequence 6167, Ap
41	74.5	7.8	789	2	US-09-949-016-9432	Sequence 9432, Ap
42	74.5	7.8	908	2	US-09-949-016-8542	Sequence 8542, Ap
43	74.5	7.8	1403	2	US-09-262-537-6	Sequence 6, Appl
44	74.5	7.8	1531	2	US-09-949-016-6740	Sequence 6740, Ap
45	74	7.7	653	2	US-09-252-991A-27553	Sequence 27553, A

## ALIGNMENTS

RESULT 1  
US-09-895-834-5  
; Sequence 5, Application US/09895834  
; Patent No. 6927040  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Haldeman, Betty A.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
; FILE REFERENCE: 01-18  
; CURRENT APPLICATION NUMBER: US/09/895,834  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/285,424  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/215,446  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-895-834-5

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Best Local Similarity 99.4%; Pred. No. 5.3e-99;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	GPVPTSKPTTGGCHIGRFSKLSPOELASFKKARDALLESILKNWSCSSPVFPQNWDL	61
Db	20	GPVTSKPTTGGCHIGRFSKLSPOELASFKKARDALLESILKNWSCSSPVFPQNWDL	79
QY	62	RLQVRPVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHLSLQACIQOPTAG	121
Db	80	RLQVRPVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHLSLQACIQOPTAG	139
QY	122	PRPGRHLHRLHQEAPKKSAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES	181
Db	140	PRPGRHLHRLHQEAPKKSAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES	199
QY	182	T 182	
Db	200	T 200	

RESULT 2  
US-09-895-834-7

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; Sequence 7, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-7

Query Match      99.0%; Score 945; DB 2; Length 200;
Best Local Similarity 99.4%; Pred. No. 5.3e-99;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 61
Db      20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 79

Qy      62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      80 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

Qy      122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 199

Qy      182 T 182
Db      200 T 200

RESULT 3
US-09-893-737-268
; Sequence 268, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-268

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Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 61
Db      20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 79

Qy      62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      80 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

Qy      122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 199

Qy      182 T 182
Db      200 T 200

RESULT 4
US-09-895-834-2
; Sequence 2, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-2

Query Match      98.4%; Score 940; DB 2; Length 200;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 61
Db      20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFPGNWDL 79

Qy      62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      80 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

Qy      122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 199

Qy      182 T 182
Db      200 T 200

RESULT 5
US-09-895-834-12
; Sequence 12, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
```

APPLICANT: Grant, Francis J.  
FILE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
CURRENT APPLICATION NUMBER: US/09/895,834  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 60/285,424  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/215,446  
PRIOR FILING DATE: 2000-06-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 203  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-895-834-12

Query Match 98.4%; Score 940; DB 2; Length 203;  
Best Local Similarity 98.9%; Pred. No. 2e-98;  
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GVPVTSKPTTGKGCHIGRFSLSPOELASFVKARDALLESLSKKNWSCSSPVFPGNWDL 61  
DB 23 GVPVTSKPTTGKGCHIGRFSLSPOELASFVKARDALLESLSKKNWSCSSPVFPGNWDL 62  
QY 62 RLLQVRERVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
DB 83 RLLQVRERVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 142  
QY 122 PRPRGLHHWLHRLQEPKESAGCLEASVTNLFRLTRDLKYVADGNLSLTSTHPES 181  
DB 143 PRPRGLHHWLHRLQEPKESAGCLEASVTNLFRLTRDLKYVADGNLSLTSTHPES 202  
QY 182 T 182  
DB 203 T 203

RESULT 6  
US-09-895-834-9  
Sequence 9, Application US/09895834  
Patent No. 6927040  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Preenelli, Scott R.  
APPLICANT: Fox, Brian A.  
APPLICANT: Gilbert, Teresa  
APPLICANT: Haldeman, Betty J.  
APPLICANT: Grant, Francis J.  
FILE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
CURRENT APPLICATION NUMBER: US/09/895,834  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 60/285,424  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/215,446  
PRIOR FILING DATE: 2000-06-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 219  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-895-834-9

Query Match 98.4%; Score 940; DB 2; Length 219;  
Best Local Similarity 98.9%; Pred. No. 2.2e-98;  
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GVPVTSKPTTGKGCHIGRFSLSPOELASFVKARDALLESLSKKNWSCSSPVFPGNWDL 61  
DB 39 GVPVTSKPTTGKGCHIGRFSLSPOELASFVKARDALLESLSKKNWSCSSPVFPGNWDL 98

QY 62 RLLQVRERVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
DB 99 RLLQVRERVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 158  
QY 122 PRPRGLHHWLHRLQEPKESAGCLEASVTNLFRLTRDLKYVADGNLSLTSTHPES 181  
DB 159 PRPRGLHHWLHRLQEPKESAGCLEASVTNLFRLTRDLKYVADGNLSLTSTHPES 218  
QY 182 T 182  
DB 219 T 219

RESULT 7  
US-09-538-092-1365  
Sequence 1365, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Giot, Loic  
APPLICANT: Mansfield, Traci A.  
FILE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CurapatSeqformat Version 0.9  
SEQ ID NO 1365  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number Q92696  
US-09-538-092-1365

Query Match 8.7%; Score 83; DB 2; Length 567;  
Best Local Similarity 25.6%; Pred. No. 1.4;  
Matches 50; Conservative 16; Mismatches 59; Indels 70; Gaps 9;  
QY 25 SPOELASFVKAR-DALLESLSKKNWSCSSPVFPGNWDLRLLOVRERPA-LEAEALTLK 82  
DB 81 SPEELAAVLKAEGLFLESLRV-----NPKSYGTWHRCWLGLRLEPNWTRLELCAR 134  
QY 83 VLE-----AAAGPALEDVLDQPLHTLH-----HLSQLQACIQOP 117  
DB 135 FLEVDERNFHCWYRRFVATQAAPAEELAFDTSLITRNFNSYSSWHYRSCLLPOLHPQ 194  
QY 118 PTAGPRPRGRLL-----HHWLHRLQEPKESACCL--- 147  
DB 195 PDGSG--PQRLPEDVLLKELELVQNAFTDPNDQSAWFYHRWL--LGRADPDQALRCLHV 250  
QY 148 ---EASVTNLFRL 159  
DB 251 SRDEACTVTSFRPL 265

RESULT 8  
US-09-370-398-6  
Sequence 6, Application US/09370398  
Patent No. 6423682  
GENERAL INFORMATION:  
APPLICANT: Ballinger, Dennis G.  
APPLICANT: Montgomery, Julie R.  
FILE OF INVENTION: Growth Factor Antagonist Materials and Methods  
FILE REFERENCE: 28110/35878  
CURRENT APPLICATION NUMBER: US/09/370,398  
CURRENT FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 13



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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17764
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: UNSURE
; LOCATION: (17)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-17764

Query Match      8.5%; Score 81.5; DB 2; Length 1228;
Best Local Similarity 33.0%; Pred. No. 5.9;
Matches 32; Conservative 5; Mismatches 33; Indels 27; Gaps 5;

QY 56 PGNWDLRL-----LQVRPVALEAEALTLKVAAGPALELDVLDQPLHTLHIL 107
Db 738 PGRADLRPADRRHHPLQRRSPVARRS-----GHARGQA--PVLDAPGSAH--- 784

QY 108 SOLQACIQQP-----TAGPRGRHLHHLHRLHRLQEAAPK 140
Db 785 --LRAAVPORGHADROPDARRRLRHRLHRLHRLHRLPR 819

RESULT 13
US-10-104-047-3099
; Sequence 3099, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3099
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3099

Query Match      8.5%; Score 81; DB 2; Length 164;
Best Local Similarity 24.3%; Pred. No. 0.41;
Matches 41; Conservative 21; Mismatches 59; Indels 48; Gaps 9;

QY 1 MGPVPTSKPTTGKGGCHGRKSLSPQELASFKK-----ARDALAESLKNWSSSPVF 55
Db 6 LSPGPVSRVLAAPSPCG-----LLEECHTLEREILLIQRCLSEBYLR-----PCH 53

QY 56 PGNWDLRL--LQVRPVALEAEALTLKVAAGPALELDVLDQPLHTLHILSOLA- 112
Db 54 PSEAALEPTLAEKEQKAMEQE-----LQASVGPSCV----SPNHRQPLGSGTQGL 102

QY 113 -----CTOPQTAGP--RPRGR--LHHWLHRLQEAAPKESA 144
Db 103 RPPLPLCGVAPLQCLPAPPLPYLRPGQSAATHRWQLQCSPPREGA 151

RESULT 14
US-08-061-636-2
; Sequence 2, Application US/08061636
; Patent No. 5858765
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: Maduale, Pascal
; TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESS: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center, 80 South Eighth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5858765West Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061.636
; FILING DATE: 12-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 9399.38-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-061-636-2

Query Match      8.4%; Score 80; DB 1; Length 563;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;

QY 16 CHIGRFKSLSPQELASFKKARDALAESLKNWSSSPVFPGNWLRLQVRPVALEA 75
Db 319 CHLGNK-----RDFVTDGFKDIWSLGVTLY-----CLLYNELPFFGEN 358

QY 76 ELAULTKVLEAAA-----GPALEDVL-----DQPLHTLHHI 106
Db 359 EFETHKIIIVLSLSSKINGNTLNDLVIKRLLEKQVTLRISIQDLVKVLSRDQPIDSRNH- 417

QY 107 LSQLO-QACIQPQTAGPRPR--GRHLHHLHRLQEAAPKESAG 145
Db 418 -SQISSSVNPNVTEGPVRRPFGRL-----LTKGKKKTSQ 452

RESULT 15
PCT-US94-05268-2
; Sequence 2, Application PC/TUS9405268
; GENERAL INFORMATION:
; APPLICANT: Iowa State University Research
; APPLICANT: Foundation, Inc.
; APPLICANT: Institut Pasteur
; APPLICANT: Institut National de la Sant et de la
; APPLICANT: Recherche M dicale
; APPLICANT: Myers, Alan M.
; APPLICANT: Maduale, Pascal
; TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center, 80 South Eighth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/061,636
; FILING DATE: 12 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueing, Ann M. and Raasch, Kevin W.
; REGISTRATION NUMBER: 33,977 and 35,651
; REFERENCE/DOCKET NUMBER: 900.39WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-05268-2

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Query Match      8.4%; Score 80; DB 4; Length 563;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;

Qy 16 CHIGRFKSLSPQELASFKKARDALFEESLKKNWSCSPVFFGNWDLRLQLQVRRPVALEA 75
Db 319 CHLGNSK-----RDFVTDGFKLDIWSLGVTLY-----CLLYNELPFFGEN 358

Qy 76 ELALTLYLEAAA-----GPALEDVL-----DQPLHTLHHI 106
Db 359 EFETVHKIIEVSLSSKINGNTLNDIVIKRLLEKDVTLRISIQDLVKVLSRDQPIDSRNH- 417

Qy 107 LSQI-QACIQOPTAGPRPR--GRLLHWLRLQEPAPKESAG 145
Db 418 -SQISSSVNPNVTEGVRPFGRLL-----LTKGKKKTSQ 452

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Search completed: December 29, 2005, 14:00:44  
Job time : 47 sec



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:59:18 ; Search time 164 Seconds  
(without alignments)  
463.689 Million cell updates/sec

Title: US-10-691-923-34  
Perfect score: 955  
Sequence: 1 MGPVPTSKPTTGKCHIGR.....LKYVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	955	100.0	182	4	US-10-691-923-34
2	955	100.0	182	5	US-10-914-772-29
3	951	99.6	182	5	US-10-914-772-41
4	950	99.5	181	4	US-10-691-923-32
5	950	99.5	181	5	US-10-914-772-27
6	950	99.5	182	4	US-10-691-923-38
7	950	99.5	182	5	US-10-914-772-15
8	948	99.3	183	5	US-10-914-772-151
9	947	99.2	183	5	US-10-914-772-155
10	946	99.1	181	5	US-10-914-772-40
11	946	99.1	182	5	US-10-914-772-85
12	946	99.1	185	5	US-10-914-772-161
13	945	99.0	182	5	US-10-914-772-89
14	945	99.0	200	3	US-09-895-834-5
15	945	99.0	200	3	US-09-895-834-7
16	945	99.0	200	4	US-10-691-923-20
17	945	99.0	200	4	US-10-790-996-5
18	945	99.0	200	4	US-10-790-996-7
19	945	99.0	200	5	US-10-928-539-5
20	945	99.0	200	5	US-10-928-539-7
21	945	99.0	200	5	US-10-914-772-4
22	945	99.0	200	5	US-10-927-891-5
23	945	99.0	200	5	US-10-927-891-7
24	945	99.0	200	5	US-10-927-815-5
25	945	99.0	200	5	US-10-927-815-7
26	944	98.8	182	5	US-10-914-772-105
27	941	98.5	181	5	US-10-914-772-83

28	941	98.5	182	5	US-10-914-772-153	Sequence 153, App
29	941	98.5	182	5	US-10-914-772-157	Sequence 157, App
30	940	98.4	180	5	US-10-914-772-139	Sequence 139, App
31	940	98.4	181	5	US-10-914-772-87	Sequence 87, Appl
32	940	98.4	182	5	US-10-914-772-97	Sequence 97, Appl
33	940	98.4	200	3	US-09-895-834-2	Sequence 2, Appli
34	940	98.4	200	3	US-09-893-737-268	Sequence 268, App
35	940	98.4	200	4	US-10-127-815-5	Sequence 5, Appli
36	940	98.4	200	4	US-10-420-034A-55	Sequence 55, Appl
37	940	98.4	200	4	US-10-691-923-4	Sequence 4, Appli
38	940	98.4	200	4	US-10-790-996-2	Sequence 2, Appli
39	940	98.4	200	5	US-10-928-539-2	Sequence 2, Appli
40	940	98.4	200	5	US-10-927-891-2	Sequence 2, Appli
41	940	98.4	200	5	US-10-927-815-2	Sequence 2, Appli
42	940	98.4	200	5	US-10-970-713-268	Sequence 268, App
43	940	98.4	203	3	US-09-895-834-12	Sequence 12, Appl
44	940	98.4	203	4	US-10-790-996-12	Sequence 12, Appl
45	940	98.4	203	5	US-10-928-539-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-10-691-923-34  
; Sequence 34, Application US/10691923  
; Publication No. US20040138122A1  
; GENERAL INFORMATION:  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Sivakumar, Pallavur V.  
; APPLICANT: Kindsvogel, Wayne R.  
; APPLICANT: Henderson, Katherine E.  
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION  
; TITLE OF INVENTION: USING IL-28 AND IL-29  
; FILE REFERENCE: 02-24  
; CURRENT APPLICATION NUMBER: US/10/691,923  
; CURRENT FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 60/420,714  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/463,939  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/420,713  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/463,982  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: met IL-29 mutant C172S  
US-10-691-923-34

Query Match	100.0%	Score 955;	DB 4;	Length 182;
Best Local Similarity	100.0%	Pred. No. 1.4e-86;		
Matches 182;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGPVPTSKPTTGKCHIGRFSKLSPOELASPKARDALAEESLKNWSSSPVFGNWD	60	
Db	1	MGPVPTSKPTTGKCHIGRFSKLSPOELASPKARDALAEESLKNWSSSPVFGNWD	60	
QY	61	LRLLQVREPPVALEALATLKVLEAAAGPALEDVLDPLHTLHHTLSQACIQOPTA	120	
Db	61	LRLLQVREPPVALEALATLKVLEAAAGPALEDVLDPLHTLHHTLSQACIQOPTA	120	
QY	121	GRPRGRHLHRLHRLQEAPEKESAGCLEASVTFNFLRLTRDLKYVADGNLSLRTSTHPE	180	
Db	121	GRPRGRHLHRLHRLQEAPEKESAGCLEASVTFNFLRLTRDLKYVADGNLSLRTSTHPE	180	
QY	181	ST 182		



Query Match 99.5%; Score 950; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.3e-86;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNWDL 61  
DB 1 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNWDL 60

QY 62 RLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
DB 61 RLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 120

QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPS 181  
DB 121 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPS 180

QY 182 T 182  
DB 181 T 181

## RESULT 5

US-10-914-772-27  
; Sequence 27, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung  
; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: 03-10  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; PRIOR FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US 60/493,194  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: US 60/551,841  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR APPLICATION NUMBER: US 60/559,142  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-29 mutant C17S  
US-10-914-772-27

Query Match 99.5%; Score 950; DB 5; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.3e-86;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNWDL 61  
DB 1 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNWDL 60

QY 62 RLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
DB 61 RLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 120

QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPS 181  
DB 121 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPS 180

QY 182 T 182

DB 181 T 181

## RESULT 6

US-10-691-923-38  
; Sequence 38, Application US/10691923  
; Publication No. US20040138122A1  
; GENERAL INFORMATION:  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Sivakumar, Pallavur V.  
; APPLICANT: Kindvogel, Wayne R.  
; APPLICANT: Henderson, Katherine E.  
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION  
; FILE REFERENCE: 02-24  
; CURRENT APPLICATION NUMBER: US/10/691,923  
; CURRENT FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 60/420,714  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/463,939  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/420,713  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/463,982  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: met IL-29  
US-10-691-923-38

Query Match 99.5%; Score 950; DB 4; Length 182;  
Best Local Similarity 99.5%; Pred. No. 4.3e-86;  
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNW 60  
DB 1 MGPVPTSKPTTGGCHIGRFSLSPOELASFKKARDALBESLKLKNWSCSSPVFFGNW 60

QY 61 LRLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120  
DB 61 LRLQVRRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120

QY 121 GPRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180  
DB 121 GPRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180

QY 181 ST 182  
DB 181 ST 182

## RESULT 7

US-10-914-772-15  
; Sequence 15, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung  
; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: 03-10  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; CURRENT FILING DATE: 2004-08-09



Db 122 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 181  
Qy 181 ST 182  
Db 182 ST 183

## RESULT 10

US-10-914-772-40  
; Sequence 40, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung  
; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: IL-29  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US 60/493,194  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: US 60/551,841  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR APPLICATION NUMBER: US 60/559,142  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (171)...(171)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val or Asn  
US-10-914-772-40

Query Match 99.1%; Score 946; DB 5; Length 181;  
Best Local Similarity 99.4%; Pred. No. 1.le-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWDL 61  
Db 1 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWDL 60  
Qy 62 RLQVRRPVALEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTAG 121  
Db 61 RLQVRRPVALEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTAG 120  
Qy 122 PRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 181  
Db 121 PRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180  
Qy 182 T 182  
Db 181 T 181

## RESULT 11

US-10-914-772-85  
; Sequence 85, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung

; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: IL-29  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US 60/493,194  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: US 60/551,841  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR APPLICATION NUMBER: US 60/559,142  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Met IL29 mutant Asp170, C172X  
; NAME/KEY: VARIANT  
; LOCATION: (172)...(172)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
US-10-914-772-85

Query Match 99.1%; Score 946; DB 5; Length 182;  
Best Local Similarity 98.9%; Pred. No. 1.le-85;  
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWD 60  
Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWD 60  
Qy 61 LRLQVRRPVALEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTA 120  
Db 61 LRLQVRRPVALEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTA 120  
Qy 121 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180  
Db 121 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180  
Qy 181 ST 182  
Db 181 ST 182

## RESULT 12

US-10-914-772-161  
; Sequence 161, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung  
; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: IL-29  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US 60/493,194  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: US 60/551,841  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR APPLICATION NUMBER: US 60/559,142  
; PRIOR FILING DATE: 2004-04-02

NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 161  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal  
; OTHER INFORMATION: Met, C175X  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (175)...(175)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
US-10-914-772-161

Query Match 99.1%; Score 946; DB 5; Length 185;  
Best Local Similarity 99.4%; Pred. No. 1.1e-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 61  
Db 5 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 64  
QY 62 RLLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
Db 65 RLLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 124  
QY 122 PRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 181  
Db 135 PRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 184  
QY 182 T 182  
Db 185 T 185

RESULT 13  
US-10-914-772-89  
; Sequence 89, Application US/10914772  
; Publication No. US20050037012A1  
; GENERAL INFORMATION:  
; APPLICANT: Brady, Lowell J.  
; APPLICANT: Klucher, Kevin M.  
; APPLICANT: Chan, Chung  
; APPLICANT: Dong, Dennis L.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bukowski, Thomas R.  
; TITLE OF INVENTION: HOMOGENEUS PREPARATIONS OF IL-28 AND  
; FILE REFERENCE: IL-29  
; CURRENT APPLICATION NUMBER: US/10/914,772  
; PRIOR FILING DATE: 2004-08-09  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Met IL29 mutant T11P, Asn170, C172X  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (172)...(172)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
US-10-914-772-89

Query Match 99.0%; Score 945; DB 5; Length 182;  
Best Local Similarity 98.9%; Pred. No. 1.4e-85;  
Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 60  
Db 1 MGVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 60  
QY 61 LRLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120  
Db 61 LRLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120  
QY 121 GPRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180  
Db 121 GPRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180  
QY 181 ST 182  
Db 181 ST 182

RESULT 14  
US-09-895-834-5  
; Sequence 5, Application US/09895834  
; Publication No. US20020039763A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Haldeman, Betty A.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
; FILE REFERENCE: 01-18  
; CURRENT APPLICATION NUMBER: US/09/895,834  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/285,424  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/215,446  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-895-834-5

Query Match 99.0%; Score 945; DB 3; Length 200;  
Best Local Similarity 99.4%; Pred. No. 1.5e-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 61  
Db 20 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 79  
QY 62 RLLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121  
Db 80 RLLQVRERPVVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139  
QY 122 PRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 181  
Db 140 PRPRGRHLHWLRHQEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 199  
QY 182 T 182  
Db 200 T 200

RESULT 15  
US-09-895-834-7  
; Sequence 7, Application US/09895834  
; Publication No. US20020039763A1

GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Haldeman, Betty A.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
; FILE REFERENCE: 01-18  
; CURRENT APPLICATION NUMBER: US/09/895,834  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/285,424  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/215,446  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-895-834-7

Query Match 99.0%; Score 945; DB 3; Length 200;  
Best Local Similarity 99.4%; Pred. No. 1.5e-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKWSKSSPVPPGNWDL 61  
DB 20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKWSKSSPVPPGNWDL 79  
QY 62 RLQVREPVVAELALTLKVLAAAGPALEDVLDPLHTLHHLSQLQACIQOPTAG 121  
DB 80 RLQVREPVVAELALTLKVLAAAGPALEDVLDPLHTLHHLSQLQACIQOPTAG 139  
QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLTSTHPES 181  
DB 140 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLTSTHPES 199  
QY 182 T 182  
DB 200 T 200

Search completed: December 29, 2005, 14:13:28  
Job time : 165 secs